

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 03:48:38 ; Search time 10747 Seconds
(without alignments)
11760.816 Million cell updates/sec

Title: US-09-730-559B-7

Perfect score: 4343

Sequence: 1.atggacgccccaaagcagg.....attcacagcagtcctctct 4343

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_em.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_rn.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	3301.2	76.0	169377	9	AC027228 Homo sapi
C 2	1420.4	32.7	1546	9	BC017880 Homo sapi
C 3	1023	23.6	2389	9	HM19880A Homo sapi
C 4	1023	23.6	3280	6	AX400060 Human iron-
C 5	990	22.8	2867	6	AX377520 Sequence
C 6	990	22.8	2867	9	HSU20180 Human iron-
C 7	944.2	21.7	3341	9	AK027033 Homo sapi
C 8	877.2	20.2	3770	6	AX377522 Sequence
C 9	877.2	20.2	3770	10	U20181 Rattus norv
C 10	396.2	9.1	309662	2	AC004469 Homo sapi
C 11	385.4	8.9	176314	2	AC044886 Homo sapi
C 12	381.2	8.8	141037	9	AC096711 Homo sapi
C 13	380.2	8.8	183658	2	AC032021 Homo sapi
C 14	380.2	8.8	186131	2	AL158192 Human DNA
C 15	377.6	8.7	170881	2	AC122718 Homo sapi
C 16	377.2	8.7	92702	9	AC091829 Homo sapi
C 17	374.6	8.6	206454	9	AC018737 Homo sapi
C 18	373.6	8.6	110000	2	Continuation (6 of
C 19	373.6	8.6	162609	9	AC108022 Homo sapi
C 20	372.2	8.6	40182	9	AC092824 Homo sapi
C 21	372.2	8.6	159385	9	AC007619 Homo sapi
C 22	371	8.5	155862	9	AC018464 Homo sapi
C 23	370.8	8.5	186321	9	AC006511 Homo sapi
C 24	369	8.5	170330	9	AC092896 Homo sapi
C 25	367.6	8.5	102837	9	HS52202
C 26	367.2	8.5	177647	9	AC091969 Homo sapi
C 27	366.8	8.4	99781	9	AF031078 Homo sapi
C 28	366.8	8.4	112756	9	AF030876 Homo sapi
C 29	364.4	8.4	195342	9	AC009120 Homo sapi
C 30	364	8.4	166032	2	AC023645 Homo sapi
C 31	363.6	8.4	86441	2	AL390762 Homo sapi
C 32	363.6	8.4	100000	9	AP000519 Homo sapi
C 33	363.6	8.4	162227	9	AB023056 Homo sapi
C 34	363.4	8.4	156399	9	AC002456 Homo sapi
C 35	361.8	8.3	175789	2	AP000425 Homo sapi
C 36	361.6	8.3	21896	9	AL591364 Human DNA
C 37	360.6	8.3	153221	2	AC067998 Homo sapi
C 38	360	8.3	134026	2	AC069317 Homo sapi
C 39	359.4	8.3	131928	9	AC091738 Homo sapi
C 40	358.4	8.3	219357	9	AC107464 Homo sapi
C 41	358.2	8.2	160302	2	AC129730 Homo sapi
C 42	358.2	8.2	193970	2	AL357119 Homo sapi
C 43	356.6	8.2	116400	9	AC055752 Homo sapi
C 44	356.6	8.2	152528	2	AC016063 Homo sapi
C 45	355.6	8.2	162232	9	AC094095 Homo sapi

ALIGNMENTS

RESULT 1
AC027228/c
LOCUS AC027228 Homo sapiens chromosome 15, clone RP11-650L12, complete sequence.
DEFINITION AC027228
ACCESSION AC027228
VERSION AC027228.16 GI:22024598
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 169377)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 15, clone RP11-650L12
JOURNAL Unpublished

REFERENCE
AUTHORS

2 (bases 1 to 169377)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collins,S., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Doming,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRoque,K., Lamazares,J., Landers,T., Lehoczeky,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Norman,C.H., Peterson,K., Pierre,N.,
Pisan,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission

TITLE
JOURNAL

Submitted (28-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 169377)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collamore,A.,
Cooke,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRoque,K.,
Lamazares,R., Landers,T., Lehoczeky,J., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Marquis,N.,
Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Nicoll,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

TITLE
JOURNAL

Submitted (12-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 169377)

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collamore,A.,
Cooke,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

TITLE
JOURNAL

Submitted (31-JUL-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE
AUTHORS

5 (bases 1 to 169377)

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collamore,A.,
Cooke,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

TITLE
JOURNAL

Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jul 31, 2002 this sequence version replaced gi:21392498.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www.seq.wi.mit.edu

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information

Center project name: L8639

Center clone name: 650_L_12

FEATURES
source

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RESULT 2

LOCUS BC017880 1546 bp mRNA linear PRI 06-DEC-2001
DEFINITION Homo sapiens, clone MGC:22754 IMAGE:4277855, mRNA, complete cds.
ACCESSION BC017880
VERSION BC017880.1 GI:17389723
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1546)
AUTHORS Strausberg,R.

TITLE
JOURNAL

REMARK
COMMENT

Direct Submission
Submitted (03-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcdepaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 35 Row: k Column: 1
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, similarity but not identity to protein.

FEATURES

Location/Qualifiers

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RESULT 3

HUMIREBPA

LOCUS

DEFINITION Human iron-responsive element-binding protein/iron regulatory protein 2 (IRE-BP2/IRP2) mRNA, partial cds.

ACCESSION M59511 M37836

VERSION M59511.1 GI:897825

KEYWORDS RNA regulatory protein; iron-responsive element-binding protein.

SOURCE Human cDNA to mRNA.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Rouault,T.A., Tang,C.K., Kaptain,S., Burgess,W.H., Haile,D.J., Samanigo,F., McBride,O.W., Harford,J.B. and Klausner,R.D.

TITLE Cloning of the cDNA encoding an RNA regulatory protein--the human iron-responsive element-binding protein

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (20), 7958-7962 (1990)

MEDLINE 91045916

PUBMED 2172968

REFERENCE

AUTHORS Rouault,T.A., Haile,D.J., Iwai,K., Rouault,T.A. and Klausner,R.D.

TITLE Molecular characterization of a second iron-responsive element-binding protein, iron regulatory protein 2. Structure, function, and post-translational regulation

JOURNAL J. Biol. Chem. 269 (49), 30904-30910 (1994)

MEDLINE 95074121

PUBMED 7983023

REFERENCE

AUTHORS Rouault,T.A., Haile,D.J., Downey,W.E., Philpott,C.C., Tang,C., Samanigo,F., Chin,J., Paul,T., Orloff,D., Harford,J.B. et al.

TITLE An iron-sulfur cluster plays a novel regulatory role in the iron-responsive element binding protein

JOURNAL Biometals 5 (3), 131-140 (1992)

MEDLINE 93044098

PUBMED 1421965

REFERENCE

AUTHORS Rouault,T.A.

TITLE Direct Submission

JOURNAL Submitted (17-DEC-1990) Tracey A. Rouault, Cell Biology and Metabolism Branch, NICHD, NIH, Bethesda, MD 20992, USA

COMMENT On Jul 14, 1995 this sequence version replaced gi:186547.

FEATURES

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BASE COUNT 879 a 534 c 637 g 839 t

ORIGIN

Query Match 23.6%; Score 1023; DB 9; Length 2889;
Best Local Similarity 100.0%; Pred. No. 6.8e-205;
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Sequence 231 from Patent WO0218424.
ACCESSION AX400060
VERSION AX400060.1 GI:21336471
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Tang,Y.T., Asundi,V., Zhou,P., Xue,A.J., Ren,F., Zhang,J.,
Wang,J.R., Zhao,Q.A., Wang,D., Liu,C., Drmanac,R.T. and Wehrman,T.
TITLE Nucleic acids and polypeptides
JOURNAL Patent: WO 0218424-A 231 07-MAR-2002;
HYSEQ, INC. (US)
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ORIGIN

Query Match 23.6%; Score 1023; DB 6; Length 3280;
Best Local Similarity 100.0%; Pred. No. 6.8e-205;
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
AX377520
LOCUS Sequence 17 from Patent WO0212284.
DEFINITION AX377520
ACCESSION AX377520
VERSION AX377520.1 GI:19573708

KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1
AUTHORS Kirsch, W.M., Lennart, A., Kellin, W.J., Kang, D.K., Levine, R.L. and Roualt, T.A.
TITLE Iron regulating protein-2 (irp-2) as a diagnostic for neurodegenerative disease
JOURNAL Patent: WO 021284-A 17 14-FEB-2002;
Loma Linda University Medical Center (US) ; THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
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Query Match 22.8%; Score 990; DB 6; Length 2867;
Best Local Similarity 100.08; Pred. No. 5.9e-198;
Matches 990; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 6
LOCUS HSU20180 2867 bp mRNA linear PRI 26-OCT-1995
DEFINITION Human iron-regulatory protein 2 (IRP2) mRNA, partial cds.
ACCESSION U20180
VERSION U20180.1 GI:897580
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 2867)
AUTHORS Guo, B., Brown, F.M., Phillips, J.D., Yu, Y. and Leibold, E.A.
TITLE Characterization and expression of iron regulatory protein 2 (IRP2). Presence of multiple IRP2 transcripts regulated by intracellular iron levels
JOURNAL J. Biol. Chem. 270 (28), 16529-16535 (1995)
MEDLINE 95348066
PubMed 7622457
REFERENCE 2 (bases 1 to 2867)
AUTHORS Brown, F.M.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-1995) Fritz M. Brown, Program in Hum. Mol. Biol. and Genetics, University of Utah, 3250 Bldg 533, Salt Lake City, UT 84112, USA
FEATURES Location/Qualifiers
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BASE COUNT 871 a 527 c 630 g 839 t
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QY 994 TCCATAGATGTTGTTCTTGGTATTACAAAG 1023
DB 961 TCCATAGATGTTGTTCTTGGTATTACAAAG 990
RESULT 7
AK027033
LOCUS
DEFINITION Homo sapiens cDNA: FLJ23380 fis, clone HEP16267, highly similar to HUMIREBPA Human iron-responsive element-binding protein/iron regulatory protein 2 (IRE-BP2/IRP2) mRNA.
ACCESSION AK027033.1 GI:10440047
VERSION
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens hepatoma cell_line:HepG2 cDNA to mRNA, clone_lib:HEP clone:HEP16267.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (sites)
Kawabata,A., Hikiiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 3341)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing; Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).
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Best Local Similarity 99.7%; Pred. No. 2.6e-188;
Matches 946; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Sequence 19 from Patent WO0212284.			
AX377522			
VERSION			
AX377522.1 GI:19573709			
KEYWORDS			
SOURCE			
Norway rat.			
ORGANISM			
Rattus norvegicus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
Rattus.			
REFERENCE			
AUTHORS			
Kirsch,W.M., Lennart,A., Kelln,W.J., Kang,D.K., Levine,R.L. and			
Roualt,T.A.			
TITLE			
Iron regulating protein-2 (irp-2) as a diagnostic for			

neurodegenerative disease		Patent: WO 0212284-A 19 14-FEB-2002;	
Loma Linda University Medical Center (US) : THE SECRETARY OF THE		DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)	
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ORIGIN			
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Db 107586 GGTGGATCATGAGTTCAGGAGATCGAGACCATCTGGCTTAACAAAGTGAACCCCGTCTC 107527
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RESULT 15
LOCUS AC122718
DEFINITION Homo sapiens chromosome 5 clone RP11-631M6, WORKING DRAFT SEQUENCE,
6 unordered pieces.
AC122718
VERSION AC122718.1 GI:21206281
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 170881)
DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
2 (bases 1 to 170881)
DOE Joint Genome Institute.
DIRECT SUBMISSION
SUBMITTED (25-MAY-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
CENTER: Joint Genome Institute
CENTER CODE: JGI
WEB SITE: http://www.jgi.doe.gov

Project Information
Center Project Name: 1537102
Center clone name: RPCI-11_631M6

Summary Statistics
Consensus quality: 164809 bases at least Q40
Consensus quality: 167217 bases at least Q30
Consensus quality: 168217 bases at least Q20
Estimated insert size: 104870; agarose-fp estimation
Estimated insert size: 170381; sum-of-contigs estimation
Quality coverage: 10.06 in Q20 bases; agarose-fp estimation
Quality coverage: 6.19 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 4603: contig of 4603 bp in length
* 4604 4703: gap of unknown length
* 4704 11301: contig of 6598 bp in length
* 11302 11401: gap of unknown length
* 11402 25882: contig of 14481 bp in length
* 25883 25982: gap of unknown length
* 25983 56850: contig of 30868 bp in length
* 56851 56951: gap of unknown length
* 56951 104415: contig of 47465 bp in length
* 104416 104515: gap of unknown length
* 104516 170881: contig of 66366 bp in length.
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/chromosome="5"
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BASE COUNT 51417 a 34652 c 33285 g 50952 t 575 others

ORIGIN

Query Match 8.7%; Score 377.6; DB 2: Length 170881;
Best Local Similarity 59.8%; Pred. No. 4.6e-69; Indels 28; Gaps 5;
Matches 734; Conservative 1; Mismatches 465;

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Qy 2359 ATTTGGTTGTATATATCTATCTGTGTTTCTTTCATCCCTAAAAATAAAMACATAGCCG 2418
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Db 750 GCAGGAGATGCGGTGAACCGGGAGCGGAGCTTGCGAGTGAGCCAAAGATTGGCCACTG 809
Qy 2659 CAGTCCGCGAGTCCGGCTTGGCGAGAGGAGACTCTGTCTCAAAAAAATAAAAAA 2718
Db 810 CAGTCCGCGAGTCCGGCTTGGCGAGAGGAGACTCTGTCTCAAAAAAATAAAAAA 869
Qy 2719 AAAAAA-----ACATAATGAGGAACGCACTCTTACACTTAGGGTTT 2763
Db 870 AAAAAATTTCTACTGAGAAACACTACTACTTTTACTGACACCTAAGAAATTGCCAGATA 929
Qy 2764 GAGTTTCTGTATCTATAAAAAAGGTTTGGATTAAGTGATCCCTGGCACTTATAAAATGT 2823
Db 930 AATGTTCTCTTCTTGTCTAAACAGAGCTCTTTGATCTTTGCTGGTAAGAAATCTTCTG 989
Qy 2824 TAGGGCTTAAATATATTCATAGATCGAGAGTAGTTTCAATCTTATAGTCGCCCTCTAGTCA 2883
Db 990 AACTGAATAAAGTTTTTGAACATGCTATGCTGTGAAAGTATACATAGCCCTTTGAGT 1049
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Qy 3182 AACACCACCTGTTTATGCACTCTAAGAAAGAAATAAGGGCTGTGTGAGTGGCT----- 3236
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Search completed: February 28, 2003, 09:06:10
Job time : 12406 secs

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Qy 3355 GCGGTGGCACATGCCCTGTAGTTCAGCTACTCTGGAGGCTAAGGTGGGAGGATTGCTAGA 3414
Db 1526 GTGGCGGCAGGCACCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATGCGCTGA 1585
Qy 3415 GCACCGGTGTTGGAAGCTGCAATGAGCTGTGACCAACACCACTGCGCTCCAGCGTGGGCAA 3474
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Qy 3475 CAGAGTGAGACCCCTGTTTCTTAAAGAAA 3502
Db 1646 CAGAGTGAGACTCCCGTCTCAAAAAAATA 1673

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 03:57:48 ; Search time 813 Seconds
(without alignments)
12030.048 Million cell updates/sec

Title: US-09-730-559B-7

Perfect score: 4343

Sequence: 1 atggagcccccacaaagcagg.....attcacagcagtcctctct 4343

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	4341.8	100.0	4343	21	AAx82629 Human IgA nephropathy-associated protein; diagnosis; treatment; antisense;
2	990	22.8	2867	24	AAD31616 Human wild-type IR
3	877.2	20.2	3770	24	AAD31617 Rat wild-type IRp
4	469.6	10.8	608	23	ABV56155 Human prostate exp
5	345.8	8.0	16511	22	AA536564 Human cardiovascular
6	336.4	7.7	237326	19	AAV57903 Hereditary haemoch
7	334.4	7.7	9840	22	AAK67429 Human immune/haema
8	327.6	7.5	10127	22	AAK78818 Human immune/haema
9	324.6	7.5	11125	22	AAK66446 Human immune/haema

C 10	322.8	7.4	235033	19	AAV57926 Hereditary haemoch
C 11	7831	7.4	235033	19	AAV57926 Hereditary haemoch
C 12	320.6	7.4	23075	22	ABA19111 Human nervous syst
C 13	317.4	7.3	465237	24	ABQ87681 Human nervous syst
C 14	317.4	7.3	465237	24	ABQ87681 Human nervous syst
C 15	314.8	7.2	57144	22	AAK79963 Human oestrogen re
C 16	314.6	7.2	27579	22	AAK79963 Human immune/haema
C 17	314.2	7.2	27579	22	AAK79963 Human immune/haema
C 18	313	7.2	154902	24	AAQ88198 Human osteoblast d
C 19	313	7.2	27960	22	AAK69779 Human immune/haema
C 20	312	7.2	27960	22	AAK69779 Human immune/haema
C 21	311.8	7.2	12355	22	AAK67628 Human immune/haema
C 22	311.8	7.2	698	22	AAK81472 Human immune/haema
C 23	311.8	7.2	38653	22	AAK81472 Human LEKTI DNA cl
C 24	311.8	7.2	368004	24	ABL57909 Human transporter
C 25	311.2	7.2	23855	22	AAI99411 Human excretory re
C 26	311.2	7.2	23855	22	AAI99411 Human kidney relat
C 27	311.2	7.2	42738	22	AAK68992 Human immune/haema
C 28	311	7.2	49634	24	ABL68647 Kidney cancer rela
C 29	311	7.2	4534	20	AAK03042 Human IL-lra BAC c
C 30	311	7.2	14991	22	AAK33441 DNA encoding human
C 31	311	7.2	20210	22	AAK77417 Human immune/haema
C 32	311	7.2	20210	22	AAK77417 Human DNA for a no
C 33	310.4	7.1	1009	22	AAK03199 Human polynucleoti
C 34	310.2	7.1	3024	22	AAH17662 Human reproductive
C 35	310.2	7.1	172637	24	ABN83124 Human cDNA sequenc
C 36	310	7.1	333	22	AAK81556 Human voltage-acti
C 37	310	7.1	26241	22	ABAI6222 Human immune/haema
C 38	309.8	7.1	32204	22	ABAI6222 Human nervous syst
C 39	309.8	7.1	32204	22	ABAI6222 Human reproductive
C 40	309.6	7.1	13873	22	ABL98413 Human testicular a
C 41	309.6	7.1	175737	22	AAK83571 DNA encoding novel
C 42	309.2	7.1	27007	22	AAK83571 DNA encoding novel
C 43	309	7.1	8639	20	AAK02995 Human IL-lra BAC c
C 44	308.8	7.1	340	22	AAK82948 Human immune/haema
C 45	307.8	7.1	10339	22	AAK82948 DNA encoding human

ALIGNMENTS

RESULT 1

AAx82629
ID AAX82629 standard; cDNA; 4343 BP.

XX AAX82629;

AC AAX82629;

DT 10-NOV-2000 (first entry)

XX Human IgA nephropathy-associated cDNA INM063-7.

DE IgA nephropathy-associated protein; diagnosis; treatment; antisense;

XX human; INM063-7; ss.

OS Homo sapiens.

XX Key

PH Location/Qualifiers

FT 1..1032

FT /*tag= a

FT /product= "INM063-7"

XX W09963085-A1.

XX 09-DEC-1999.

XX 28-MAY-1999; 99WO-JP02855.

XX 02-JUN-1998; 98JP-0152603.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;

XX Sawada S, Takei M, Shibata K, Furuya A;

XX WPI; 2000-097328/08.
DR P-PSDB; AAW90743.

XX DNA sequences preferentially expressed in IgA nephropathy patients,
PT proteins encoded by them, and antibodies to those proteins -
XX
PS Claim 1; Page 106-113; 180pp; Japanese.

XX This invention describes novel DNA sequences preferentially expressed in
CC IgA nephropathy patients, and DNA sequences stringently hybridizing to
CC them. Independent claims cover diagnostic reagents for IgA nephropathy
CC incorporating the antisense sequences; the treatment of IgA nephropathy
CC using the antisense sequences for mRNA inhibition; proteins associated
CC with IgA nephropathy, containing sequences encoded by the DNA sequences;
CC antibodies recognizing these proteins; the production of the proteins
CC by culture of host cells transformed with DNA encoding them; diagnostic
CC reagents for IgA nephropathy containing the antibodies; and compositions
CC for the treatment of IgA nephropathy which contain the antibodies. The
CC products of the invention can be used for the diagnosis and treatment of
CC IgA nephropathy. This sequence encodes the human IgA
CC nephropathy-associated protein INN063-7 which is described in the
CC method of the invention.

XX Sequence 4343 BP; 1321 A; 795 C; 865 G; 1359 T; 3 other;

Query Match 100.0%; Score 4341.8; DB 21; Length 4343;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	361	CGGACAGATCTTACAGTTGACCATTTTCAAAATGACTTCAGTAAATGTCGAATACAG	420
Db	361	CGGACAGATCTTACAGTTGACCATTTTCAAAATGACTTCAGTAAATGTCGAATACAG	420
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Db	421	AATGACCAAAATCCTGGAGGTGGTACCTGCAGAAAGCAGGAAAGCTCTCCACTTAAA	480
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Db	481	GTGACGCTTAAGAAGCTTCCCTGCAGAGGCCAGACTACCTCCGAGGATCTGTGATTCT	540
Qy	541	GGAGAACTAGGCCGAAACTCAGGAACATTTTCTTCGAGATTTGAGATACACCCATCCTG	600
Db	541	GGAGAACTAGGCCGAAACTCAGGAACATTTTCTTCGAGATTTGAGATACACCCATCCTG	600
Qy	601	TGTCCTTTTCAATTTGCAACACAGTGCCTGAACCTGAAACAGTGTAAAAAATCAAGAAGTA	660
Db	601	TGTCCTTTTCAATTTGCAACACAGTGCCTGAACCTGAAACAGTGTAAAAAATCAAGAAGTA	660

Qy	661	GAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTTTAACTGGAGTTCAAGAGTTTTAAAG	720
Db	661	GAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTTTAACTGGAGTTCAAGAGTTTTAAAG	720
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Qy	781	TCAGAGTGGTTTTTCAAGAAAAAGACCTCCTCTCCACAGACAGTCTAGTCGGCACAGAT	840
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Qy	841	TCACACATCAACGATGATGATGTTTAGGATTTCTGGGCTGGGGGTTGGAGGCATTTGAA	900
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Qy	901	ACAGAGCAGTTATGCTTGGTCTGCCAGCTTCTCTTACTTTACCAGAGTGGTTGGATGT	960
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Qy	1021	AAGGTAAAGTTAAAGTTGTGTAGCTCTATGACTTACTGAACATTTATTTATAAAATTTG	1080
Db	1021	AAGGTAAAGTTAAAGTTGTGTAGCTCTATGACTTACTGAACATTTATTTATAAAATTTG	1080
Qy	1081	AAGAGCTCTATGAGACAGGATTTGGGTTTCATTTACTGCTCCTCAGGCTCTCTGACGTT	1140
Db	1081	AAGAGCTCTATGAGACAGGATTTGGGTTTCATTTACTGCTCCTCAGGCTCTCTGACGTT	1140
Qy	1141	AGCCACATCATATAGTATATAGTAATAAACAAACACAGAGCATTTAGTTTGTACTAA	1200
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Db	1201	TAAATACAAAGAAATTTGTTGTGTTTCACTTATGTTAGTCTATTTAGTCTCTATAACAAG	1260
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Qy	1381	GGCAGTCAGATTTCTGAGTCATGCTTAACCATTTATGCCCTTATTTAGTGCCTTGTGGCTTA	1440
Db	1381	GGCAGTCAGATTTCTGAGTCATGCTTAACCATTTATGCCCTTATTTAGTGCCTTGTGGCTTA	1440
Qy	1441	ATAAACACTTGTGGACTACATATTTTCTCTCTTTTAACTTCAATTAATAAATAAAT	1500
Db	1441	ATAAACACTTGTGGACTACATATTTTCTCTCTTTTAACTTCAATTAATAAATAAAT	1500
Qy	1501	GTTTAGCAAAAGTTGATGTTGCTCTTTAAATTAATTTATTTGCCCGTTAGAACTGTTG	1560
Db	1501	GTTTAGCAAAAGTTGATGTTGCTCTTTAAATTAATTTATTTGCCCGTTAGAACTGTTG	1560
Qy	1561	CTCTACTAAGTAATGCTTTTCAAAACATGGACTGTAGAATGTGATATATCATTTTCTG	1620
Db	1561	CTCTACTAAGTAATGCTTTTCAAAACATGGACTGTAGAATGTGATATATCATTTTCTG	1620
Qy	1621	TTGCCGTTTTTAACATTTCTCTGGAATTTATGTAAAAATCTTCTCTGAATTTTAAAA	1680
Db	1621	TTGCCGTTTTTAACATTTCTCTGGAATTTATGTAAAAATCTTCTCTGAATTTTAAAA	1680
Qy	1681	TACTGGCTTCAGAACTTCAATACATACACTGAGCTGTTTAAAGCATATTAAACACAGGCT	1740
Db	1681	TACTGGCTTCAGAACTTCAATACATACACTGAGCTGTTTAAAGCATATTAAACACAGGCT	1740

QY 1741 CACGGATTCCTAGTGACAAATAATTTGTAACTCTTCTCCTAAATGCTGGCCTTTGCT 1800
DB 1741 CACGAAATTCCTAGTGAACAATAATTTGTAACCTCTTCTCCTAAATGCTGGCCTTTGCT 1800
QY 1801 AACTTTATTTAAATGATTAAATCCTATTCTTTGTTAAATGAATGTACCTGGAAATGTTCCA 1860
DB 1801 AACTTTATTTAAATGATTAAATCCTATTCTTTGTTAAATGAATGTACCTGGAAATGTTCCA 1860
QY 1861 CATATAATCCAAATTTGAGTCCCAATCTCAGCAATTTTGGTTAGATTATTTGGTACGAAGG 1920
DB 1861 CATATAATCCAAATTTGAGTCCCAATCTCAGCAATTTTGGTTAGATTATTTGGTACGAAGG 1920
QY 1921 CTTTCTGGATACCTCCAGTGTAAAGAAATGATAATGCGCTCCCTCTCACCAATTTGGTATTGA 1980
DB 1921 CTTTCTGGATACCTCCAGTGTAAAGAAATGATAATGCGCTCCCTCTCACCAATTTGGTATTGA 1980
QY 1981 TCCTTCTCCCTAAATAGAAAAGAAATTTGGCATCTTAGAGAAATATTGATTCAACGTAT 2040
DB 1981 TCCTTCTCCCTAAATAGAAAAGAAATTTGGCATCTTAGAGAAATATTGATTCAACGTAT 2040
QY 2041 GATACCAAAAGATCAAGTAGTAATAATTTGGGAATTCGAGGATTATTCCTAGAGGAAAAGGAG 2100
DB 2041 GATACCAAAAGATCAAGTAGTAATAATTTGGGAATTCGAGGATTATTCCTAGAGGAAAAGGAG 2100
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DB 2101 TATCCCATATTGTTTTACAGAAATCAATCTTTTACTTTTAGACATCCTGAAAACACTAACGC 2160
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DB 2161 TGCCTTTTGTAGCCTTCTCTAGCTGTTTTTCTGACAAATATTACTGTGTGTTTTTGTACAT 2220
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DB 2221 TTTAGTTTAAATGTTTAAAAAATTAATCTATTATATATGTTTACATTATTTCGAATATTGA 2280
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DB 2281 TTACTCTCTTTTTCAGATCCTGTTCCAATTTGTGATCCTTATAGAAATAATCCTGTATTGT 2340
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DB 2341 TTTTTTGTATGAGACAGCATTTGGTTTGTAAATATCTAATCTGTGTTCTTTTCATCCTAAA 2400
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DB 2401 AAATAAAACCATAGCCGGCGGGGTGGCTCACGCCCTGTAATCCCAGCACTTTTGGAGGC 2460
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DB 2581 GCTTCTCGGAGGCTGAGGCAGGAGAAATGGCGTGAACCCGGGAGGGAGCTTSCAGTGA 2640
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DB 2641 GCCAAGATTGGCCACTGCACTCCGAGTCGGCAGTCGGCCTGGGGGACAGAGCAGACTCTGT 2700
QY 2701 CAAAAAATAAAAAAAAAAAAAACCAATAATAGAGAAACGCATCTTTTACACTTAGGG 2760
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DB 3001 CACATGTTTAAACAAATCTACCAAGTGGGATTTGCCCTGTGATTAAAGATGCTGTAAACAT 3060
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DB 3121 TATACAGTTTTCATCAGTCTATTAGTATTTCATTAAGTCTTAAGATGCCATCAGTGGTTAGC 3180
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DB 3301 AACATTGTAAAGACCCCTGTCTCTACAAAAAAGTTTAAAAATTTAGTGGTGGCTGGTG 3360
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DB 3541 TGAGTTGAGGTACCCCTGATTTCAAAGACATGAAAAATGTTTAAATATAGCCACCTTGAAGCT 3600
QY 3601 TTTCAGGSCCCTTTCTACCTGAAATTAACAGTGACATTTGGACCAGTCTTCTCTTTACTTCT 3660
DB 3601 TTTCAGGSCCCTTTCTACCTGAAATTAACAGTGACATTTGGACCAGTCTTCTCTTTACTTCT 3660
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DB 3661 TATCTTAAATAACCCCAAAACAGAAATGAGTTGATTTCATAGGACAAATGAAGGATCTCA 3720
QY 3721 TTTCTTCACCATCAGTATGTTGGTTTAAAAATTTTATTTATAGTTTTCAGACAAATCGTT 3780
DB 3721 TTTCTTCACCATCAGTATGTTGGTTTAAAAATTTTATTTATAGTTTTCAGACAAATCGTT 3780
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DB 3781 GCTAATCTTATCTTTGCAATTTTGTATGTTTCTGTATTTCCCTATATAGCACCCTCAG 3840
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DB 3841 GCAAGTAGGAGTGGCTGAAAGTTTGTTCAGTTTTTTTGGAAAGTGGAGTTTTCACAAATATC 3900
QY 3901 TATAGTTGATCGAACTACAATAGCAAAACATGTGTCGGGAATATGTTGCTATCCTCAGCTT 3960
DB 3901 TATAGTTGATCGAACTACAATAGCAAAACATGTGTCGGGAATATGTTGCTATCCTCAGCTT 3960

Db 3901 TATAGTTGATCGAACTACAAATAGCAACATGTGTCCGGAAATATGGTGTATCTCCACGCTT 3960
Qy 3961 TTTCCCTGTTGACAAATGTGACATTAACATTTAGAACATACAGGTAAAGAGATAAAGA 4020
Db 3961 TTTCCCTGTTGACATGTGACATTAACATTTAGAACATACAGGTAAAGAGATAAAGA 4020
Qy 4021 TCACAGATAAACAATGTACATTTCCAAATGTGTTTGAATAATTTATAAATTTACTACC 4080
Db 4021 TCACAGATAAACAATGTACATTTCCAAATGTGTTTGAATAATTTATAAATTTACTACC 4080
Qy 4081 TTATCATGTATTTTACTACACAAAATTTACATATGTTTCAACACAACTTTCAAGCA 4140
Db 4081 TTATCATGTATTTTACTACACAAAATTTACATATGTTTCAACACAACTTTCAAGCA 4140
Qy 4141 AACATCAGATGCTTTTAAAGAGTGTGTGCTCAAAACCTTAGTTCCTGTGACACATTTG 4200
Db 4141 AACATCAGATGCTTTTAAAGAGTGTGTGCTCAAAACCTTAGTTCCTGTGACACATTTG 4200
Qy 4201 AAAGCAATTTAAAGGAATTTATTCAAACCATTTGATCTGACTGTTTCCCATATGA 4260
Db 4201 AAAGCAATTTAAAGGAATTTATTCAAACCATTTGATCTGACTGTTTCCCATATGA 4260
Qy 4261 TGGATACCTCCCTCTACTTAGGGGTCATAGGTGCAATTTTAAATGGAGTCAGCCCTTAA 4320
Db 4261 TGGATACCTCCCTCTACTTAGGGGTCATAGGTGCAATTTTAAATGGAGTCAGCCCTTAA 4320
Qy 4321 CATATTCACAGCGTCCCTTCT 4343
Db 4321 CATATTCACAGCGTCCCTTCT 4343

RESULT 2
AAD31616
ID AAD31616 standard; cDNA; 2867 BP.
XX
AC AAD31616;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human wild-type IRP-2 protein encoding cDNA.
XX
KW Human; iron regulating protein-2; mild cognitive impairment syndrome;
KW IRP-2 peptide loop; neurodegenerative disease; Alzheimer's disease;
KW MCI; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2859
FT /*tag= a
FT /product= "Human wild-type IRP-2 protein"
FT /note= "CDS does not include start codon"
FT /partial
XX
PN WO200212284-A2.
XX
PD 14-FEB-2002.
XX
PF 06-AUG-2001; 2001WO-US24747.
XX
PR 04-AUG-2000; 2000US-222863P.
XX
PA (UYLO-) UNIV LOMA LINDA MEDICAL CENT.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kirsch WM, Lennart A, Kelln WJ, Kang D, Levine RL, Roualt TA;
XX
DR WPI; 2002-241735/29.
DR P-PSDB; AAE19851.
XX
PT New iron regulating protein-2 polypeptides and polynucleotides, useful
PT as diagnostic for neurodegenerative diseases, particularly Alzheimer's
PT disease

XX Disclosure; Page 59; 65pp; English.
PS
XX
CC The invention relates to nucleic acid molecule which encode a peptide
CC loop corresponding to amino acid residues 136-216 of human wild-type
CC iron regulating protein-2 (IRP-2). IRP-2 proteins are unable to undergo
CC oxidation at critical cysteine residues and are diagnostic for neuro-
CC degenerative disease. The invention also provides nucleic acid fragments
CC encoding mutant IRP-2 proteins. The mutation interferes with the ability
CC of a cysteine residue present in the peptide loop to undergo oxidation.
CC The IRP-2 is useful as a diagnostic for neurodegenerative diseases
CC including Alzheimer's disease and mild cognitive impairment syndrome
CC (MCI). Mutant IRP-2 proteins may be used in generating probes for the
CC diagnosis of neurodegenerative diseases and in generating antibodies
CC which bind to an epitope present on the mutant polypeptide. The present
CC sequence is a cDNA encoding human wild-type IRP-2 protein.
XX
SQ Sequence 2867 BP; 871 A; 527 C; 630 G; 839 T; 0 other;

Query Match 22.8%; Score 990; DB 24; Length 2867;
Best Local Similarity 100.0%; Pred. No. 1.7e-177;
Matches 990; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 TACCTATTGCAACATTAATGACAGTTCACATAAAGATTTCTTCGATGTATCTAACTT 93
Db 1 TACCTATTGCAACATTAATGACAGTTCACATAAAGATTTCTTCGATGTATCTAACTT 60
Qy 94 GGCACCAAGTATGATGTTCTGCTTACTCAATACGGGTCTTGTGGAAGCTGCTGACGA 153
Db 61 GGCACCAAGTATGATGTTCTGCTTACTCAATACGGGTCTTGTGGAAGCTGCTGACGA 120
Qy 154 AATTGTGATGGCTTTTAAATGAAGAAGAGATGTTATGAACATTTTAGACGTGGAACCC 213
Db 121 AATTGTGATGGCTTTTAAATGAAGAAGAGATGTTATGAACATTTTAGACGTGGAACCC 180
Qy 214 AAACAAGCAATGTTGAAGTCCCTTTTCCCTGCCCGTCTTCTTCAAGATTTTACT 273
Db 181 AAACAAGCAATGTTGAAGTCCCTTTTCCCTGCCCGTCTTCTTCAAGATTTTACT 240
Qy 274 GGAATACCAGCAATGTTGGATTTTGTGCTATGAGGAGGAGCACTTCTTGAGGT 333
Db 241 GGAATACCAGCAATGTTGGATTTTGTGCTATGAGGAGGAGCACTTCTTGAGGT 300
Qy 334 GATCCTGAGAAAGTCCATCTGCTGTGTCGACAGATCTTACAGTTGACCATTTTACAA 393
Db 301 GATCCTGAGAAAGTCCATCTGCTGTGTCGACAGATCTTACAGTTGACCATTTTACAA 360
Qy 394 ATTGACTTCAGTAATGTCGAATACAGAATGCACAAATCCTCGAGTGGTGACCTGCAG 453
Db 361 ATTGACTTCAGTAATGTCGAATACAGAATGCACAAATCCTCGAGTGGTGACCTGCAG 420
Qy 454 AAAGCAGGAAAGCTCTCTCCACTTAAAGTGCAGCCTAAGAAGCTTCCCTGCAGAGCCAG 513
Db 421 AAAGCAGGAAAGCTCTCTCCACTTAAAGTGCAGCCTAAGAAGCTTCCCTGCAGAGCCAG 480
Qy 514 ACTACCTGCCGAGATCTTGTGATTTGGAGAACTAGGCCGAACTCAGGAACATTTTCT 573
Db 481 ACTACCTGCCGAGATCTTGTGATTTGGAGAACTAGGCCGAACTCAGGAACATTTTCT 540
Qy 574 TCGCAGATTGAGAAATACACCCATCTCTGCTTTCATTTGCAACAGCTGCAACCT 633
Db 541 TCGCAGATTGAGAAATACACCCATCTCTGCTTTCATTTGCAACAGCTGCAACCT 600
Qy 634 GAAACAGTGTATAAATAAAGAGTAGAATTCGGCAGAAATCGAGAGGCTTCAGTTT 693
Db 601 GAAACAGTGTATAAATAAAGAGTAGAATTCGGCAGAAATCGAGAGGCTTCAGTTT 660
Qy 694 TTTAAGTGGAGTTCAGAGATTTTAAAGAAATGTCGACGTGATCCCTCTGAACTGGATG 753
Db 661 TTTAAGTGGAGTTCAGAGATTTTAAAGAAATGTCGACGTGATCCCTCTGAACTGGATG 720
Qy 754 GCTCATCAATAAATTTAGAAATATTTGTCGAAGTGGTGTGGAAGAAAGACCTCCTC 813
Db 720

Db 721 GCTCATCAATAAACTTAGAATATTGTCAGAGTGGTTTTTGAAGAAAAAGACCTCCTC 780

Qy 814 TTCCACACAGTGTAGTCGCGACAGATTTCACACATAAAGATGGTGAATGGTTAGGGATT 873

Db 781 TTCCACACAGTGTAGTCGCGACAGATTTCACACATAAAGATGGTGAATGGTTAGGGATT 840

Qy 874 CTGGGTGGGGGTGGAGGCATTGAACAGAGCAGTATGCTTGGTCTGCCAGTTTCT 933

Db 841 CTGGGTGGGGGTGGAGGCATTGAACAGAGCAGTATGCTTGGTCTGCCAGTTTCT 900

Qy 934 CTTACTTTACCAGAGTGGTGGATGTGAGTTAACTGGGTCAATCAACCCCTTTTGTACA 993

Db 901 CTTACTTTACCAGAGTGGTGGATGTGAGTTAACTGGGTCAATCAACCCCTTTTGTACA 960

Qy 994 TCCATAGATGTTGTTCTTGGTATTACAAAG 1023

Db 961 TCCATAGATGTTGTTCTTGGTATTACAAAG 990

RESULT 3

AAD31617

ID AAD31617 standard; cDNA; 3770 BP.

XX

AC AAD31617;

XX

DT 18-JUN-2002 (first entry)

XX

DE Rat wild-type IRP-2 protein encoding cDNA.

XX

KW Rat; iron regulating protein-2; mild cognitive impairment syndrome;

KW IRP-2 peptide loop; neurodegenerative disease; Alzheimer's disease;

KW MCI; ss.

XX

OS Rattus norvegicus.

XX

FH Key

FT CDS

FT Location/Qualifiers

FT 12..2903

FT /*tag= a

FT /product= "Rat wild-type IRP-2 protein"

XX

PN W0200212284-A2.

XX

PD 14-FEB-2002.

XX

PF 06-AUG-2001; 2001WO-US24747.

XX

PR 04-AUG-2000; 2000US-222863P.

XX

PA (UYLO-) UNIV IOWA LINDA MEDICAL CENT.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Kirsch WM, Lennart A, Kellin WJ, Kang D, Levine RL, Roualt TA;

XX

DR WPI; 2002-241735/29.

DR P-PSDB; AAE19852.

XX

PT New iron regulating protein-2 polypeptides and polynucleotides, useful

PT as diagnostic for neurodegenerative diseases, particularly Alzheimer's

PT disease

XX

PS Disclosure; Page 62-63; 65pp; English.

XX

CC The invention relates to nucleic acid molecule which encode a peptide

CC loop corresponding to amino acid residues 136-216 of human wild-type

CC iron regulating protein-2 (IRP-2). IRP-2 proteins are unable to undergo

CC oxidation at critical cysteine residues and are diagnostic for neuro-

CC degenerative disease. The invention also provides nucleic acid fragments

CC encoding mutant IRP-2 proteins. The mutation interferes with the ability

CC of a cysteine residue present in the peptide loop to undergo oxidation.

CC The IRP-2 is useful as a diagnostic for neurodegenerative diseases

CC including Alzheimer's disease and mild cognitive impairment syndrome

CC (MCI). Mutant IRP-2 proteins may be used in generating probes for the

CC diagnosis of neurodegenerative diseases and in generating antibodies

CC which bind to an epitope present on the mutant polypeptide. The present

CC sequence is a cDNA encoding rat wild-type IRP-2 protein.

XX

SQ Sequence 3770 BP; 1119 A; 713 C; 840 G; 1098 T; 0 other;

Query Match 20.2%; Score 877.2; DB 24; Length 3770;

Best Local Similarity 91.6%; Pred. No. 3 4e-156;

Matches 940; Conservative 0; Mismatches 83; Indels 3; Gaps 1;

Qy 1 ATGGAGGCCCAAAAGCAGGATACGCCCTTTGAGTACCTTATTGAAACATTAATGACAGT 60

Db 12 ATGGAGTCCCAAGTGCAGGATACCTTTGAGTACCTTATTGAAACATTAATGACAGT 71

Qy 61 TCACATAAGAAAGTCTTCGATGTATCTAAACTTT---GGCACCAAGTATGATGCTTGCGCT 117

Db 72 TCACAGAAGAAGTCTTCAATGTACCTAACTTGGAGGCCACCAAGTATGATATCTGCT 131

Qy 118 TACTCAATACGGGCTTGTGGAAGCTGCTAGCAAAATTTGATGGCTTTTAAATGAAG 177

Db 132 TACTCAATACGGGCTTGTGGAAGCTGCTAGCAAAATTTGATGGCTTTTAAATGAAG 191

Qy 178 AAGGAAGATGTTATGAACATTTAGACTGGAAAAACCAAAAGCAATTTGAAAGTGCC 237

Db 192 AAGGAAGATGTTATGAATATTTGGACTGGAAAAACCAAAAGCAATTTGAAAGTGCC 251

Qy 238 TTTTCCCTGCCGCTGTTCTTCAAGATTTTACTGGAATACCAAGTGGTGGATTT 297

Db 252 TTTTCCCTGCCGCTGTTCTTCAAGATTTTACTGGAATACCAAGTGGTGGATTT 311

Qy 298 GCTGCTATGAGGGAGGAGTGAACCTTGGAGGTGATCTGAGAAAGTCCATCTGCT 357

Db 312 GCTGCTATGAGGGAGGAGTGAACCTTGGAGGTGATCTGAGAAAGTCCATCTGCT 371

Qy 358 TGTCGACAGATCTTACAGTTGACCAFTTTTACAAATTTGACTTCAAGTAAATGTCAATA 417

Db 372 TGTCGACAGATCTTACAGTTGACCAFTTTTACAAATTTGACTTCAAGTAAATGTCAATA 431

Qy 418 CAGAAATGCACCAATCTCGAGGTGGTACCTGCAGAAAGCAGGAAAGCTCTCCACTT 477

Db 432 CAGAAATGCACCAATCTCGAGGTGGTACCTGCAGAAAGCAGGAAAGCTCTCCACTT 491

Qy 478 AAGTGCAGCTAAGAGCTTCCCTGCGAGGCCAGACTACCTGCCGAGGATCTTGTGAT 537

Db 492 AAGTGCAGCTAAGAGCTTCCCTGCGAGGCCAGACTACCTGCCGAGGATCTTGTGAT 551

Qy 538 TCTGGAGAACTAGGCCGAACTCAGGAACATTTCTTCGAGATTGAGAAATACACCCATC 597

Db 552 TCTGGAGAACTAGGCCGAACTCAGGAACATTTCTTCGAGATTGAGAAATACACCCATC 611

Qy 598 CTGTGCTCTTTTCATTTGCAACCAAGTCCCTGGAACCTGAGACGCTGTAATAAATCAAGAA 657

Db 612 CTGTGCTCTTTTCATTTGCAACCAAGTCCCTGGAACCTGAGACGCTGTAATAAATCAAGAA 671

Qy 658 GTAGAAATTCGACAGAAATTCGAGAGGCTTCACTTTTAAAGTGGAGTCAAGAGTTTA 717

Db 672 GTAGAAATTCGACAGAAATTCGAGAGGCTTCACTTTTAAAGTGGAGTCAAGAGTTTA 731

Qy 718 AAGAAATGTCAGTGTATCCCTCTGGAACCTGGAATGCTCATCAATAAAGTAAATAT 777

Db 732 AAGAAATGTCAGTGTATCCCTCTGGAACCTGGAATGCTCATCAATAAAGTAAATAT 791

Qy 778 TTGTCAAGAGTGGTTTTTGAAGAAAGACCTCTCTTCCAGACAGTGTAGTCCGCCACA 837

Db 792 TTGTCAAGAGTGGTTTTTGAAGAAAGACCTCTCTTCCAGACAGTGTAGTCCGCCACA 851

Qy 838 GATTTCACATATAAGCATGGTGAATGTTTGGGATTTCTGGGGTGGGGGTTGGAGGCATT 897

Db 852 GATTTCATATAAAGCATGGTGAATGTTTGGGATTTCTGGGGTGGGGTGTGGAGGCATT 911

Qy 898 GAACAGAGAGCATGTATGCTTGGTCTGCCAGTTTCTTACTTTACCAGAGTGGTTGA 957

Db 912 GAGACAGAGGCAGTATGCTTGGCTGCCAGTCTTACTTACTTTTACCAGAGTGGTTGA 971

PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
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PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
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PR 05-SEP-2000; 2000US-0229509.
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PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
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PR 08-SEP-2000; 2000US-0232080.
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PR 12-SEP-2000; 2000US-0232198.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
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PR 14-SEP-2000; 2000US-0233063.
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PR 21-SEP-2000; 2000US-0234223.
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PR 25-SEP-2000; 2000US-0234997.
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PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
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PR 29-SEP-2000; 2000US-0236327.
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PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0250390.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0251989.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-451930/48.
New cardiovascular system related polynucleotides and polypeptides, which encode the cardiovascular system antigen polypeptides of the invention.
Cardiovascular system antigens and their associated polynucleotides are useful for diagnosing, treating and/or preventing disorders of the cardiovascular system -
Claim 1; SEQ ID No 2064; 674pp; English.
Sequences AAS35741-AAS36942 represent genomic DNA molecules, which encode the cardiovascular system antigen polypeptides of the invention.
Cardiovascular system antigens and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs,

CC chickens or sheep. A pathological condition can be determined by
CC detecting the presence or absence of a mutation in a cardiovascular
CC system antigen polynucleotide. The treatable disorders include autoimmune
CC diseases such as rheumatoid arthritis, hyperproliferative disorders such
CC as neoplasms of the breast or liver, cardiovascular disorders such as
CC cardiac arrest, cerebrovascular disorders such as cerebral ischemia,
CC nervous system disorders such as Alzheimer's disease, infections caused
CC by bacteria, viruses and fungi, ocular disorders such as corneal
CC infection, endocrine disorders such as premature labour and infertility,
CC gastrointestinal disorders such as Crohn's disease, renal disorders such
CC as glomerulonephritis and respiratory disorders such as asthma and
CC pleurisy. The polypeptides can also be used to aid wound healing, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, to regenerate tissues and in chemotaxis.
CC Note: the sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

Query Match 8.0%; Score 345.8; DB 22; Length 16511;
Best Local Similarity 61.3%; Pred. No. 8.1e-56;
Matches 682; Conservative 1; Mismatches 408; Indels 22; Gaps 7;

QY 2404 TAAACCATATAGCCGGCGCGGTGCTCACGCCCTGTATCCAGCACCTTTGGGAGGCCGA 2463
DB 645 TTAATAAAGGCGGGTGGCTGCTACACCTGTATCCAGCACCTTTGGGAGGCCCTA 704
QY 2464 GCGGGTGTGATCATGAGTGCAGGAGATCGAGACCATCTCGGTCTAACAAGGTGAACCCCG 2523
DB 705 GCGGGCAGATCAGGAGTGCAGAGATCAAAACCATCTCGGTCTACACGGTGAACCCCG 764
QY 2524 TCCTCTACTAAATAACAAA--AAATAGCCGGCGCGGTGGCGGCCGCTGTAGTCCCGAG 2581
DB 765 TCCTCTACTAAATGCAAAACAAATTAGCCAGGCATGGTGGTGGCCACCTGTAGTCCCGAG 824
QY 2582 CTTCTCGGAGGTGAGGAGGAGAGATGCGTGAACCCGGGAGGCGGAGCTTGCAGTGAG 2641
DB 825 CTACTCGGAAGTGAAGGAGGAGAGATGCGTGAACCCAGGAGGAGAGCTTGCAGTGAG 884
QY 2642 CCAAGATTCGGCCACATCGAGTCGCGAGTCCGGCTGGGCGAGAGAGCTGTGTYC 2701
DB 885 CCAAGATGGCACCACT-----GCACCTCCAGCTGGGCGAGAGAGCTCCGCTC 937
QY 2702 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2761
DB 938 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 997
QY 2762 TTGAGTTTCTGATCTATAAANAAGGT--TTGGATTAAGTATCCCTGGCATTATAA 2819
DB 998 GAGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1057
QY 2820 ATGTTAGGGCTTAATATTATTCATAGATCGAGGATAGTTTCTTGTAGTCGCTCCTTA 2879
DB 1058 CAATAACATGGAATAAATTTCTCAGAAATATCAAAAGATCAAAATGAACATTTA 1117
QY 2880 GTCACCTCTTCCATACCAATCTCAGACCAATTTTACAAATTTAGAAAGACAAATACTGGT 2939
DB 1118 GATAGTTTTTCATCTACCAAAATGGAAGCATATCAAAAAAATAAGTAACTGGTCACAATGT 1177
QY 2940 TGGGTTACTTTAGTATATATACCAAGAAAAATAATTTTGAAGCAATTAAGTTTGA 2999
DB 1178 AGAGAGACTCTCAGTGAAGTCTCAATTTGTTTACCGTTTCTAGACAAATTTGAGCAGTTGT 1237
QY 3000 CCACATGTTAAACAAATTTCTACCAAGTGGGATTTGCTGTGATTAAGATGCTGTAACA 3059
DB 1238 ATTAGTTATTAANAAGTCCATGATCTATTCTGTGACCTATCTACTATTTTCCCT-GTGA 1296
QY 3060 TTTGGGCCAGTAGTATAAATTTGAAAAATGTTTATAGCAATATATAATTTTATTTAA 3119
DB 1297 TTCTTGACTTTAAATCAAACTCCCAAAATTTTGAACCTTTTGAACCTTTTGAACCTTTGA 1356
QY 3120 ATATACAGTTTCATGCTCTATTAGTATTTCATTAAGTCTTAGATCCATCATGCTGTTAG 3179

DB 1357 GTATGAATATTGACTAACAATTTGTAAAGTTGAGATGCTATGAGAATA-----TGGGAA 1412
QY 3180 CAAACACCACTGTTTATGCACTGCTAAGAAAGAAATAAAGGGCTGTGTGCACTGGCTCAC 3239
DB 1413 AATTGACATTTCTTAAGATTTATTGACTGACACAGTGGTTTACGCTGTATATCCAG 1472
QY 3240 ACCTTGGGAGCCGACAGGAGGAGCATCTCTGAGGCCAGAGATTCAAGACCAACCTGGT 3299
DB 1473 CACTTTGGGAGGCCAAGATGGGAGGATCACTTGGAGCCAGGATTCAGAACTACCCCTGG 1532
QY 3300 CAACATTTGTAAGCCCTGTCTCTACAAAAAATAAAGTTAAAAAATAGCTGGTGGT 3359
DB 1533 CAACATAGTGAGA--CCTGTCTCAACAAAAAGTAAA-----AAAAATTAACATGTTGGT 1586
QY 3360 GGACATCCCTGTAGTTCCAGCTACTCTGGAGGCTAAGGTGGGAGGATTTGCTAGAGCCAC 3419
DB 1587 GGTGATCCCTGTGTGCTCCAGCTACTTTGGAAGGCTGAGGATGAGGATCGCTTGAGACTA 1646
QY 3420 GGTGTTGGAAGCTGCAATGAGCTGTGACCAACACACTGCGCTCCAGGTGGGCAACAGAG 3479
DB 1647 GGAGATCAAGGCTGCAGTGCAGCTGTGATCATGCACTGCACCTCCAGCTGGGCAACAGAA 1706
QY 3480 TGAGACCCCTGTTCTTAAAGAAAGAAAGAAAAA 3512
DB 1707 TGAGACCCCTTCTCTAAATAAATAAATAA 1739
RESULT 6
AAV57903/c
ID AAV57903 standard; DNA: 237326 BP.
XX AC AAV57903;
XX XX
XX 21-DEC-1998 (first entry)
XX DE Hereditary haemochromatosis subregion from an HH affected individual.
XX KW Bovine butyrophilin; BF; human hereditary haemochromatosis; HFE;
XX KW diagnosis; iron metabolism; NPT3; NPT4; Rofet; BTF1; BTF2; BTF3;
XX KW BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
XX KW type 1 sodium transport gene; ss.
XX OS Homo sapiens.
XX PN WO9814466-A1.
XX XX
XX PD 09-APR-1998.
XX PF 30-SEP-1997; 97WO-US17658.
XX PR 07-MAY-1997; 97US-0852495.
XX PR 01-OCT-1996; 96US-0724394.
XX XX
XX PA (PROG-) PROGENITOR INC.
XX PI Feder JN, Kronmal GS, Lauer PM, Ruddy DA, Thomas WJ;
XX PI Tsuchihashi Z, Wolff RK;
XX XX
XX DR WPI; 1998-240014/21.
XX Hereditary haemochromatosis gene products - used to develop products
XX for the diagnosis and treatment of hereditary disorders in iron
XX PT metabolism
XX PS Claim 1; Fig 9; 209pp; English.
XX CC The present invention describes hereditary haemochromatosis gene
XX CC products from the human haemochromatosis gene. The present sequence
XX CC represents a hereditary haemochromatosis subregion from an hereditary
XX CC haemochromatosis (HH) affected individual. Also described is a
XX CC method to determine the presence or absence of the common hereditary
XX CC haemochromatosis (HFE) gene mutation in an individual comprising:
XX CC (a) providing DNA or RNA from the individual; and (b) assessing the

CC DNA or RNA for the presence or absence of a haplotype or genotype where
CC the presence or absence of the haplotype genotype indicates the likely
CC presence of the HFE gene mutation in the genome of the individual. The
CC HFE gene sequences from the present invention can be used to develop
CC products for use in the diagnosis and treatment of hFE. The present
CC invention also describes Bf genes, which are homologues of the milk
CC protein butyrophilin (Bf), and can be used in the production of agonists
CC and antagonists of Bf function. Also described are: (1) a Roret gene
CC which can be used to develop products for the study, diagnosis and
CC treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes
CC which are homologues of a type 1 sodium transport gene, and can
CC similarly be used for hypophosphatemia.
XX

XX SQ Sequence 237326 BP; 69596 A; 48904 C; 48217 G; 70609 T; 0 other;
Query Match 7.7%; Score 336.4; DB 19; Length 237326;
Best Local Similarity 59.8%; Pred. No. 8e-54;
Matches 680; Conservative 1; Mismatches 432; Indels 25; Gaps 6;

.QY 2386 TTCTTTTCATCTAAAAATAAACCATAGCCGGCGCGGTGGCTCAGCGCTCTAATCCC 2445
D 137745 TTATATTTCTTTGGATAAAGTCAGTAGCGGGCGCGGTGCTCATGCTGTGATCCT 137686
D 2446 AGCATTTTGGAGCCGAGCGGGTGGATCATGAGGTCAGGATCGAGACCATCTCTGGC 2505
D 137685 AGCATTTTGGAGGCTGAGGTGGCGAGATCATGAGGTCAGGATCGAGACCATCTCCGGC 137626
QY 2506 TAACAAGGTGAACCCGCTCTCTACTAATAAATACAAAAATTAGCCGGGGCGGTGGCGG 2565
D 137625 TAACACGGTGAACCCGCTCTCTACTAATAAATACAAAAATTAGCTGGGCGTGGCGCG 137566
QY 2566 GCGCTCTAGTCCAGCTTCTCGGAGGCTGAGCAGGAATGGCTGAACCCGGGAGG 2625
D 137565 GCGCTCTGTGTCAGCTACTCGGAGGTGAGCAGGAGATGGCGTGAATCCGGGAGG 137506
QY 2626 CGGAGCTTGCAAGTGAAGTGGCCACTGCACTCCGCGCTCGGCGTGGCGGACAG 2685
D 137505 CGGAGGTGCAAGTGAAGTGGCCACTGCACTCCGCGCTCGGCGGACAG 137453
QY 2686 AGCGAGACTCTGTCTCAAAAAAAGGAGTGGAGTGGTGGTAAAGTATGATCC 2745
D 137452 AGCGAGACTCTGTCTCAAAAAAAGGAGTGGAGTGGTGGTAAAGTATGATCC 137393
QY 2746 TCTTTACACTTAGGGTTGAGTTCTGTATCTATAAAAAAGGTTTGGATTAAGTATCC 2805
D 137392 TGCATTGCTTTGGGACTTTTAATATTAGTCTACAAATCTAGCCACCATAGAAATCTGC 137333
QY 2806 CTGGCACTTATAAATGTTAGGCTTAATATTATTCATAGATCGGAGATGTTCAATCT 2865
D 137332 TGATTAATACGGGTCTCTGTAAATGGAAACATGCAATTTTGGGGGAAAAAGAGGAGT 137273
QY 2866 TAGTCGCTCTCTTAGTCACCTCTCTCTATACCAATCTGAGACCATTTTACAATTTAGAAA 2925
D 137272 GTTTAGTGAATTTGTTTGTACACTGTTTATAATAAATTTAAGCAATCTTGAGGGG 137213
QY 2926 GACAATACTGTTGGTGTACTGTAGTATAGTATAAACAAGAAAAAATTAATTTAGAAGG 2985
D 137212 AACATTTTATTTCTACTTGTAACTGCAATAAGTTATGAGATAAAGTTACAAGCTATATCA 137153
QY 2986 AATTAAGTTTGAACACATG--TTAACAATAATCTACCAAGTGG-GAATTCGCTGTGAT 3042
D 137152 CATACAGTTTGTAGCTTTAATAATTTAATGAAATCTAACAGATAAATATGCTTAATATGAT 137093
QY 3043 TAAAGATGCTTAACATTTGGGCCAGTAGTTATATTTTGAATAATGTTTATAGCCAATA 3102
D 137092 GAAATGCTATAAATTAATAGATAGATATATTTAATAAACCAATTCAGAAAGGACCAATA 137033
QY 3103 TATAATTTTATTTAAATATACAGTTTCATCAGTCTA-----TTAGTATTTTCATTAA 3155
D 137032 CCCAATTTTCAAAATCATATTAATTTGTAATTAATTAGGCGCAGCAAAATATCTTGGAT 136973
QY 3156 GTCTAGATGCCATCAGTGGTTAGCAACACACACTGTTTTTATGCACTGCTAAGAAGAAAT 3215

D 136972 TCTTTCTAATAAACAATAAGTGTAAATACAGTCTGACTGACAAATCTGAAGAATTTATG 136913
QY 3216 AAAGGCTGTGTGCAAGTGGCTCACACCTGTGGAGCGCCAGGAGCATCAGTTGAGG 3275
D 136912 CAGCATAAAAAGTGTATATCCAGCACTTTGGGAGGCCAAGGTGGCAGATCA--TGAGG 136855
QY 3276 CCAGAAGTTTCAAGACCAACCTGTCACATTTCTCAACATTTCTAAGACCCCTCTCTCTACAAAAA 3335
D 136854 TCAGGAGTTGGAGACAGCCCTGACCAACATGTTGTAACCCCTCTTACTAAAAATA--- 136798
QY 3336 AGTTAAAAATTAGCTGGGTGGCGGTGGCAGATGCTGTAGTTCAGTCTCTGGAGGCTA 3395
D 136797 ---CAAAATTTAGCCGGGCTTGGTGGTGCACACCTGTATCCAGCTGCTCAGGAGGCTA 136741
QY 3396 AGTGGGAGGATGTAGAGCCAGCGGTGTGAAAGTGTGCAATGAGCTGTGACCAACACAC 3455
D 136740 AGGCAGGAGAACTGCTTGAATCCAGGAGGTGGAAGTTGCAGTAAGCAAGATCAGCCAC 136681
QY 3456 TCGCTCCAGCGTGGGCAACAGATGAGACCCCTGTTTCTTAAAGAAAGAAAGAAAAA 3513
D 136680 TGCATCCAGCCCTGGGCGAGAGTGTGACTCTGACTCAAAAAAATAAATAAATA 136623
RESULT 7
AAK67429
ID AAK67429 standard; DNA; 9840 BP.
XX AC AAK67429;
XX AC AAK67429;
DT 06-NOV-2001 (first entry)
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22241.
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
XX WO200157182-A2.
XX 09-AUG-2001.
XX 17-JAN-2001; 2001WO-US01354.
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.

Db 3686 AATTATAGAAAGCGCGCGGCGAGTGGCTCACACCTGTATCCAGCAGCTTTGGGAGGC 3745
QY 2461 CGAGCGGGTGGATCATGAGGTGAGGATCGAGACCTCTGGCTAACAGGTGAAGAAC 2520
Db 3746 CGAGCGGGCAGATCATGAGGTGAGGATCGAGACCTCTGGCTAACAGGTGAAGAAC 3805
QY 2521 CCGTCTCTACTATAAATACAAAAATAGCCGGGCGGCTGGCGGCGCTGTAGTCCCA 2580
Db 3806 CCGTCTCTACTATAAATACAAAAATAGCCGGGCGGCTGGCGGCGCTGTAGTCCCA 3865
QY 2581 GCTTCTCGGAGGTGAGGAGGAGAAATGGCTGAACCGGAGCGGAGCTTGCAGTGA 2640
Db 3866 GCTACTTTGGAGGTGAGGAGGAGAAATGGCATGAACCTGGGAAGCGAACTTGGAGTGA 3925
QY 2641 GCCAGATTTGGCCACTGAGTCCGAGTCCGCGCTGGCCGACAGGAGGAGCTCTGTT 2700
Db 3926 GCCAGATTTGGCCACTGAGTCCGAGTCCGCGCTGGCCGACAGGAGGAGCTCTGTT 3978
QY 2701 CAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2760
Db 3979 CAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4038
QY 2761 TTTGAGTTTCTGTATCTATAAAGAGGTTTGGATTAGTATGATCCCTGGCCTTATAAAA 2820
Db 4039 TGATGCCACACAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4096
QY 2821 TGTTAGGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2880
Db 4097 GTATAGGCTGTAGTAAATCTAGAGCTAGACTTTCTAGGATTCAGGCTGCTGTC 4156
QY 2881 TCACCTTCTCTATACCACTGAGACCATTTTACAAATTTAGAAAGACAAATAACTGGTT 2940
Db 4157 ACTTACAGCTGAGTAATTTGGGACCTGATTTAACCTCTGTTTCCTCATCTGTAAT 4216
QY 2941 GGGTACTGTAGTATATAAACAAGAAATAATTTTGAAGGAATAAGTTTGAAGAAC 3000
Db 4217 GGGATGTAATAGTA-CATATTTCCACAGGTTGGTGTAGATGGAATGAATCGATTC 4275
QY 3001 CACATGTTAAACAAATCTACCAAGTGGGATTTGCGTGTATTAAGATGCTGTAACAT 3060
Db 4276 TAAGTACGCATATATTGAATAAATCTTACTATGGAAGTTCAAACTTACAAAAAGCA 4335
QY 3061 TTGGGCCAGTAGTTTAAATTTGAAAAATGTTTATAGCCAAATATAATTTT-TTTATTT 3117
Db 4336 GAGATTACATAATGAATCCACATATTTTCACTCATCTTCGATGATCAACATTTGTT 4395
QY 3118 AAATATACAGTTTCATCAGTCTATTAGTATTTTCAATTAAGTCTAAGATGCCATCAGTGT 3177
Db 4396 GATCTTGCTATCAGCTGATTTTGCTTAGCTCATATTTTAAAGCAATCCAGACACA 4455
QY 3178 AGCAACACCACTGTTTATGCACTGCTAGAAAGAAATTAAGGCTGTGTGCACTGGGCTC 3237
Db 4456 TCATTTTACCCTATAAATATTTCCAGTATGGGCCAGGCGTGTGGCTCAGCGCTGTAATCCC 4515
QY 3238 ACACCTGTGGACGCCAGCAGGAGCATCTTGAAGGCCAGAGTTTCAAGAACCAACTG 3297
Db 4516 ACCACTTTGGAGCGGAGGCGGCGATCATTGAGTTCAGGAGTTTCGAGAGTCCCTG 4575
QY 3298 GTCAACATGTAGACCTGCTCTACAAAAAAGTTAAATTTAGTTAGTGGGTGCG 3357
Db 4576 GTCAACATGTGGGAACCTGCTCTACTAAAAAATAAAAA-AAAATTAGCCAGGCGTG 4632
QY 3358 GTGGCACATGCTGTAGTTCAGTCTCTGAGGAGTAAAGTTGGGAGGATTCGTAGAGCC 3417
Db 4633 GTGGGTGTACCTGTATCCAGCTACTCAGGAGGCTGAAGCAAGAAATCGCTTGACCC 4692
QY 3418 AGGTTGTTGAGGTGCAATGAGTGTGACCAACACACTGCGCTCCAGCGTGGGCAACAG 3477
Db 4693 CAGGAGGCGGAGGTGCGAGTGAAGCAAGATTGGGCGCACTGCACCTAAGCGCTAGGCAACAG 4752
QY 3478 AGTGAGACCCCTGTTTCTTAAAGAAAGAAAGAAAAA 3513
Db 4753 AGCAAGACCCGCTTCTTAAAAAACAATAAATACACA 4788

RESULT 8
AAK78818/c
ID AAK78818 standard; DNA; 10127 bp.
XX AC AAK78818;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33630.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
OS
XX WO200157182-A2.
XX
XX 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.

PR	08-SEP-2000;	2000US-0232081.
PR	12-SEP-2000;	2000US-0231968.
PR	14-SEP-2000;	2000US-0232397.
PR	14-SEP-2000;	2000US-0232398.
PR	14-SEP-2000;	2000US-0232399.
PR	14-SEP-2000;	2000US-0232400.
PR	14-SEP-2000;	2000US-0232401.
PR	14-SEP-2000;	2000US-0233063.
PR	14-SEP-2000;	2000US-0233064.
PR	14-SEP-2000;	2000US-0233065.
PR	21-SEP-2000;	2000US-0234223.
PR	21-SEP-2000;	2000US-0234274.
PR	21-SEP-2000;	2000US-0234275.
PR	25-SEP-2000;	2000US-0234998.
PR	25-SEP-2000;	2000US-0234999.
PR	26-SEP-2000;	2000US-0235484.
PR	27-SEP-2000;	2000US-0235834.
PR	27-SEP-2000;	2000US-0235836.
PR	29-SEP-2000;	2000US-0236327.
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PR	02-OCT-2000;	2000US-0237038.
PR	02-OCT-2000;	2000US-0237039.
PR	03-OCT-2000;	2000US-0237040.
PR	13-OCT-2000;	2000US-0239935.
PR	13-OCT-2000;	2000US-0241826.
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PR	20-OCT-2000;	2000US-0241221.
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PR	20-OCT-2000;	2000US-0241786.
PR	20-OCT-2000;	2000US-0241787.
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PR	20-OCT-2000;	2000US-0241809.
PR	20-OCT-2000;	2000US-0241826.
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PR	08-NOV-2000;	2000US-0246474.
PR	08-NOV-2000;	2000US-0246475.
PR	08-NOV-2000;	2000US-0246476.
PR	08-NOV-2000;	2000US-0246477.
PR	08-NOV-2000;	2000US-0246478.
PR	08-NOV-2000;	2000US-0246523.
PR	08-NOV-2000;	2000US-0246524.
PR	08-NOV-2000;	2000US-0246525.
PR	08-NOV-2000;	2000US-0246526.
PR	08-NOV-2000;	2000US-0246527.
PR	08-NOV-2000;	2000US-0246528.
PR	08-NOV-2000;	2000US-0246532.
PR	08-NOV-2000;	2000US-0246609.
PR	08-NOV-2000;	2000US-0246610.
PR	08-NOV-2000;	2000US-0246611.
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PR	17-NOV-2000;	2000US-0249212.
PR	17-NOV-2000;	2000US-0249214.
PR	17-NOV-2000;	2000US-0249215.
PR	17-NOV-2000;	2000US-0249216.
PR	17-NOV-2000;	2000US-0249217.
PR	17-NOV-2000;	2000US-0249218.
PR	17-NOV-2000;	2000US-0249244.
PR	17-NOV-2000;	2000US-0249245.
PR	17-NOV-2000;	2000US-0249264.
PR	17-NOV-2000;	2000US-0249265.
PR	17-NOV-2000;	2000US-0249297.
PR	17-NOV-2000;	2000US-0249299.
PR	17-NOV-2000;	2000US-0249300.

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DB 4853 CTTAATGATTGCTGATACAGGCTATTTTCATGGGAA---TCACAAAATTTGATT 4797
QY 2825 AGGCTTTAATATTATATAGATCGAGTAGTATTTTCATCTTTAGTCGCTCTTGTAGTCAC 2884
DB 4796 AAAATGATTATTTAGTTGAAAATGCACCTCGCAAGATTTTTGGGATATACCCAGCTAA 4737
QY 2885 TCCTCTTATACCACTGAGACCATTTTACAAATTTAGAAAAGACAAATAACTGTTGGGT 2944
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QY 2945 TACTTGATGATATAAATCAACCAAGAAAATAATTTTGAAGGAATTAAGTTTCAACACACA 3004
DB 4676 TACTTAAGAAGA---AACCACATAGAAATTTAGGCAAAAAGGGAAGTATGAATACAGAA 4621
QY 3005 TGTTAACAAATTTACCAAGTGGGATTTGCCTGTGATTAAGATGCTGTAAACATTTGG 3064
DB 4620 TTTAAGCCTCTATGCTAGTGTAGTATTAAGTACATTAAGATCAATTAACAGATCAATAAGTT-- 4563
QY 3065 GCCAGTAGTATATAATTTGAAAAATGTTTATAGCCAATATATATTTTATTTAAATATA 3124
DB 4562 -----CTATATGCACAGACTAATATCAAGAAATCAAGTTGAAAGAGCTCTG 4514
QY 3125 CAGTTTCATCAGTCTATTAGTATTTCAATTAAGTCTAAGATGCCATCAGTGTAGCAAC 3184
DB 4513 GAGCTTGCCCACTTAAGTCTACCCAGTGGG-----NA 4480
QY 3185 ACCACTGTTTATGCACTGCTAAGAAAGAAATAAAGGGCTGTGTGAGTGGCTCACACTG 3244
DB 4479 ATCCCTTCTCAAAATGATGGCCGGCATGTTGCTCATGCTATATGATCCAGCACTT 4420
QY 3245 TGGACGCCAAGCAGAGATCCTTGAGGCCAGAAAGTTCAAGACCAACCTGTGTCAACA 3304
DB 4419 TGGAGGCCCTAGGCAGCGGATCACTTGAGGTCAGGAGTTTGAACCCAGCCTGGCCACA 4360
QY 3305 TTGTAAAGACCTGTCTACAAAAAATAAAGTTAAATTAAGTGGTGGGTGGGCAC 3364
DB 4359 TGGTGAACCCCACTCTACTAAATAACAAACAATTAGCAGGTGTG-TGGTGGCAC 4301
QY 3365 ATGCTGTAGTTCGAGTACTCTGGAGGCTAAGTGGGAGGATTTCTAGAGCCAGGTTGT 3424
DB 4300 ACGCTCTAATCCAGTACTTGGAGGCTTAAGGCAGGAGAACTGTTGAACCCAGGAGG 4241
QY 3425 TGGAGCTGCAATGAGCTGTGACACACACCACTCGCTGAGGCTGGGCAACAGAGTGAGA 3484
DB 4240 TGGAGGTTGTTAAGCCGAGATTGTCACCTGCAATTCAGGCTAGAAAACGGAGCAAGA 4181
QY 3485 CCCTGTTCTTAAGAAGAAAGAAAAGGGCTGCGCACTTAACAGACACACTATTGAG 3544
DB 4180 CTCCATCTCAAAAACAAAAGCTAGCTAATGAAGAGCAGCTTCCACAAAATCAAAACCTAG 4121
QY 3545 TT 3546
DB 4120 CT 4119

RESULT 9
AAK66446
ID AAK66446 standard; DNA: 11125 BP.
AC AAK66446;
XX
XX
DT 06-NOV-2001 (first entry)
DE
DE
XX
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
XX
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WO200157182-A2.

09-AUG-2001.

17-JAN-2001; 2001WO-US01354.

31-JAN-2000; 2000US-0179065.

04-FEB-2000; 2000US-0180628.

24-FEB-2000; 2000US-0184564.

02-MAR-2000; 2000US-0186350.

16-MAR-2000; 2000US-0189874.

17-MAR-2000; 2000US-0190076.

18-APR-2000; 2000US-0198123.

19-MAY-2000; 2000US-0205515.

07-JUN-2000; 2000US-0209467.

28-JUN-2000; 2000US-0214886.

30-JUN-2000; 2000US-0215135.

07-JUL-2000; 2000US-0216847.

07-JUL-2000; 2000US-0216880.

11-JUL-2000; 2000US-0217487.

11-JUL-2000; 2000US-0217496.

14-JUL-2000; 2000US-0218290.

26-JUL-2000; 2000US-0220963.

14-AUG-2000; 2000US-0224518.

14-AUG-2000; 2000US-0224519.

14-AUG-2000; 2000US-0225213.

14-AUG-2000; 2000US-0225214.

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14-AUG-2000; 2000US-0225447.

14-AUG-2000; 2000US-0225757.

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22-AUG-2000; 2000US-0226681.

22-AUG-2000; 2000US-0226868.

22-AUG-2000; 2000US-0227182.

23-AUG-2000; 2000US-0227009.

30-AUG-2000; 2000US-0228924.

01-SEP-2000; 2000US-0229287.

01-SEP-2000; 2000US-0229343.

01-SEP-2000; 2000US-0229344.

05-SEP-2000; 2000US-0229345.

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06-SEP-2000; 2000US-0230437.

06-SEP-2000; 2000US-0230438.

08-SEP-2000; 2000US-0231242.

08-SEP-2000; 2000US-0231243.

08-SEP-2000; 2000US-0231244.

08-SEP-2000; 2000US-0231413.

08-SEP-2000; 2000US-0231414.

08-SEP-2000; 2000US-0232080.

08-SEP-2000; 2000US-0232081.

12-SEP-2000; 2000US-0231968.

14-SEP-2000; 2000US-0232397.

14-SEP-2000; 2000US-0232398.

14-SEP-2000; 2000US-0232399.

14-SEP-2000; 2000US-0232400.

14-SEP-2000; 2000US-0232401.

14-SEP-2000; 2000US-0233063.

14-SEP-2000; 2000US-0233064.

14-SEP-2000; 2000US-0233065.

21-SEP-2000; 2000US-0234223.

21-SEP-2000; 2000US-0234274.

25-SEP-2000; 2000US-0234997.

25-SEP-2000; 2000US-0234998.

26-SEP-2000; 2000US-0235484.

27-SEP-2000; 2000US-0235834.

27-SEP-2000; 2000US-0235836.

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 DB 9914 TTCTTAAACACAGGCGCTAGACCAAGTAGTGTAAACAGACTTCATGATTTGG 9973
 QY 3053 GTAACATTTGGGCGAGTAGTTATAATTTGAAAAAGTTTATAGCAATATATAATTTT 3112
 DB 9974 TTATTTATCTCTCTCACTAGTGTGATAGAGGGGTTTATATACAGCTTTCTTCASTGC 10033
 QY 3113 TATTTAAATATACAGTTTTCATCAGCTTATTAGTATTTCATTAAGTCTAAGATGCCATCAG 3172
 DB 10034 TGTATCCCTAATGCTTAAACAGCGCCCTGTACATACAGGCAATTCAGCTTAAACTTAT 10093
 QY 3173 TGGTTAGCAACACCATCTGTTTTATGCACTGCTAAGAAAGATAAAGGGCTGTGTCAGT 3232
 DB 10094 TGAGTAAATGAATAAGGTACACATTTATCATGAAGATTAAACGTTTGGTTGGCTTCGGGGGT 10153
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 DB 10154 GCTCAGACCTGTAATCCAGCACCTTTGGGAGCAAGGAGGCGGATCAGCTGAGGTCA 10213
 QY 3279 GAAGTTCAAGACCAACCGGTGTAACATGTGAAGACCTGTCTCTCAAAAAAAGT 3338
 DB 10214 GGAGTTCAAGACCAACCGGTGTAACATGTGAAGACCTGTCTCTCAAAAAAAGT 3338
 QY 3339 TAAAAATTAGCTGGGTGGCGGCGACATGCTGTAGTTCAGCTACTCTGGAGGCTAAG 3398
 DB 10268 CAAAATTAGCTGGGTGGCGGCGACATGCTGTAGTTCAGCTACTCTGGAGGCTAAG 3398
 QY 3399 TGGAGGAGTTGCTAGAGCCAGCGTGTGGAAGCTGCAATGAGTGTGACACACCACTGC 3458
 DB 10328 CAGGTGAATGCTTGAATCGGGAAGCAGAGGTTGCACTGAGCCACATCATGCCACTGC 10387
 QY 3459 GCTCCAGCGTGGGCAACAGAGTGAGACCGTGTCTTAAAAAGAAAGAAAGG 3515
 DB 10388 ACTCCAGTTGGGTGACAGAGGAAGTCTGTCTAGAAAAAATAAAAAAAG 10444

RESULT 10
 AAV57926/C
 ID AAV57926 standard; DNA; 235033 BP.
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 AC AAV57926;
 XX
 DT 23-DEC-1998 (first entry)
 XX
 DE Hereditary haemochromatosis subregion from an unaffected individual.
 XX
 KW Bovine butyrophilin; BF; human hereditary haemochromatosis; HFE;
 KW diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3;
 KW BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
 KW type 1 sodium transport gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9814466-A1.
 XX
 PD 09-APR-1998.
 XX
 PF 30-SEP-1997; 97WO-US17658.
 XX
 PR 07-MAY-1997; 97US-0852495.
 PR 01-OCT-1996; 96US-0724394.
 XX
 XX (PROG-) PROGENITOR INC.
 XX
 XX Feder JN, Kronmal GS, Lauer PM, Ruddy DA, Thomas WJ;
 PI Tsuchihashi Z, Wolff RK;
 XX
 XX WPI; 1998-240014/21.
 DR
 XX Hereditary haemochromatosis gene products - used to develop products
 PT for the diagnosis and treatment of hereditary disorders in iron
 PT metabolism

XX Example 2; Fig 8; 209pp; English.
 XX
 CC The present invention describes hereditary haemochromatosis gene
 CC products from the human haemochromatosis gene. The present sequence
 CC represents a hereditary haemochromatosis subregion from an individual
 CC unaffected by hereditary haemochromatosis (HH). Also described is a
 CC method to determine the presence or absence of the common hereditary
 CC haemochromatosis (HFE) gene mutation in an individual comprising:
 CC (a) providing DNA or RNA from the individual; and (b) assessing the
 CC DNA or RNA for the presence or absence of a haplotype or genotype where
 CC the presence or absence of the haplotype genotype indicates the likely
 CC presence of the HFE gene mutation in the genome of the individual. The
 CC HFE gene sequences from the present invention can be used to develop
 CC products for use in the diagnosis and treatment of HFE. The present
 CC invention also describes BTF genes, which are homologues of the milk
 CC protein butyrophilin (BF), and can be used in the production of agonists
 CC and antagonists of BF function. Also described are: (1) a RoRet gene
 CC which can be used to develop products for the study, diagnosis and
 CC treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes
 CC which are homologues of a type 1 sodium transport gene, and can
 CC similarly be used for hypophosphatemia.
 XX
 SQ Sequence 235033 BP; 69786 A; 48466 C; 49441 G; 68340 T; 0 other;
 Query Match 7.4%; Score 322.8; DB 19; Length 235033;
 Best Local Similarity 59.1%; Pred. No. 2.9e-51;
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 QY 2446 AGCACTTTGGAGCGCGAGGGGTGGATCATGAGTTCAGAGATCGAGACCACTGCTGC 2505
 DB 132329 AGCACTTTGGAGCGCGAGGGTGGATCATGAGTTCAGAGATCGAGACCACTGCTGC 132270
 QY 2506 TAACAAGGTGAACCCGCTCTCTACTAAAAATACAAAAATAGCGGGCGGCTGGCGG 2565
 DB 132269 TAACACGTTGAACCCGCTCTCTACTAAAAATACAAAAATAGCTGGGCGTGGCGG 132210
 QY 2566 CGCCTGTAGTCCAGCTTCTCGGGAGGCTGAGCGAGGAGTAATGGGTGAACCCGGAGG 2625
 DB 132209 CGCCTGTAGTCCAGCTTCTCGGGAGGCTGAGCGAGGAGTAATGGGTGAACCCGGAGG 132150
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 DB 132096 AGCAAGACTCTGTCTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 132037
 QY 2746 TCTTTACACTTAGGTTTGGTTTCTGTATCTATAAAAAAGGTTTGGATTAGTATCC 2805
 DB 132036 TGCCTTCTGCTTTGG-----GACTTTTACTATTAGTCTACAAATCTAGCCACCATAGACT 131981
 QY 2806 CTGCACTTATAAAATGTTAGGCTTAAATATTATTTATAGATCGAGGATAGTTTCTATCT 2865
 DB 131980 CTGCTGATTAAATAGGGGTTCTGTAAAAATGAAACATGCAATTTTGGGGGAAAAAGAGG 131921
 QY 2866 TAGTCGCTTCTTAGTCTACCTTCTTATACCAATCTGAGACCATTTTACAAATTAGAAAA 2925
 DB 131920 GAGTGTGTTTGTAGTATTTGTTTTTACACATGTTTATAATAAATTTTAAAGCACTCTGA 131861
 QY 2926 GACAAATAACTGTTGGGTTTACTTTAGTAGTATAATAACCAAGAAAAATAATTTTGAAGG 2985
 DB 131860 GGGGAACATTTTATTTCTACTTGTAACTGCATAAAGTTATCAGATAAGTTACACAGCTAT 131801
 QY 2986 AATTAAAGTTGAACCAACATGTTTACAAATTTTACCAAAAGTGGGATTTGCTGTGATTA 3045
 DB 131800 ATCATAACAGTTTGTAGCTTTTATAAATTTATGAATTTTAACTTCTAACAGACTAAATGCTACTA 131741

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 20-OCT-2000; 2000US-0242221.
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 08-NOV-2000; 2000US-0246476.
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 08-NOV-2000; 2000US-0246523.
 08-NOV-2000; 2000US-0246524.
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 17-NOV-2000; 2000US-0249216.
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 17-NOV-2000; 2000US-0249244.
 17-NOV-2000; 2000US-0249245.
 17-NOV-2000; 2000US-0249264.
 17-NOV-2000; 2000US-0249265.
 17-NOV-2000; 2000US-0249266.
 17-NOV-2000; 2000US-0249297.
 17-NOV-2000; 2000US-0249299.
 01-DEC-2000; 2000US-0250391.
 01-DEC-2000; 2000US-0251160.
 05-DEC-2000; 2000US-0251030.
 05-DEC-2000; 2000US-0251988.
 06-DEC-2000; 2000US-0256719.
 08-DEC-2000; 2000US-0251479.
 08-DEC-2000; 2000US-0251856.
 08-DEC-2000; 2000US-0251868.
 08-DEC-2000; 2000US-0251989.
 08-DEC-2000; 2000US-0251990.
 11-DEC-2000; 2000US-0254097.
 05-JAN-2001; 2001US-02559678.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-541565/60.
 Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 useful for preventing, diagnosing and/or treating nervous system
 cancers and metastases -
 Disclosure; SEQ ID NO 11442; 1701pp + Sequence Listing; English.
 The invention relates to novel genes (AB11004-AB21534) and proteins
 (AB14678-AB18001) useful for preventing, treating or ameliorating
 medical conditions e.g. by protein or gene therapy. The genes are
 isolated from a range of human tissues disclosed in the specification.
 The nucleic acids, proteins, antibodies and (ant)agonists are useful
 in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 and ovarian cancer and other cancers of the adrenal gland, bone, bone

marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 and parasitic infections.
 Note: The sequence data for this patent did not form part of the
 printed specification, but was obtained in electronic format directly
 from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 7831 BP; 2347 A; 1433 C; 1460 G; 2591 T; 0 other;

Query Match 7.4%; Score 320.6; DB 22; Length 7831;
 Best Local Similarity 59.2%; Pred. No. 4e-51;
 Matches 680; Conservative 1; Mismatches 420; Indels 48; Gaps 6;

QY 2385 TTTCTTTCATCTTAAATAAACCATAGGCGGCGGCTGCTCAGCGCTGTATTC 2444
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 QY 2445 CAGCACTTTGGAGCGCGGCTGATCATGAGTTCAGGATCGAGACCATCTGG 2504
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 QY 2906 CCATTTTACAAATTTAGAAAGACAAATAAAGTGGTTGGTTTCTGTATGATATATATACCA 2965
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 Db 4690 TTATGGAATTTTAGCCCAAAATTTACTTTTAAACAATTTGGGCTTAGATGTAACCTCATG 4631
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 QY 3086 AATGTTTATAGCCCAATATATAATTTTAAATATAACAGTTTCAATCATGCTTATAGT 3145
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QY	3206	AAGAAAGATAAAGGCTGTGTGCACT-GGCTCACACCTGTGGAGCCCAAGGCAGGAGC	3264	PR	14-AUG-2000;	2000US-0225214.
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Db	4524	CGCCAGGCCAGTGGCTCATGCCTGTAAATCCAGCACTCTGGAGGCTGACGGGGTGG	4465	PR	14-AUG-2000;	2000US-0225267.
Db	4524	CGCCAGGCCAGTGGCTCATGCCTGTAAATCCAGCACTCTGGAGGCTGACGGGGTGG	4465	PR	14-AUG-2000;	2000US-0225270.
QY	3265	ATCACTTGAGCGCCAGAAGTTCAAGACCAACCTGGTCAACATTTGAAGACCCCTGTCTCTAC	3324	PR	14-AUG-2000;	2000US-0225447.
Db	4464	ACTGCTTGAGCGCCAGGAGTTTGACAGCAGCCTGGCCAAACATGGTGAACACCGCTCTGCAC	4405	PR	14-AUG-2000;	2000US-0225757.
QY	3325	AAAAAAAAGTTAAAAATTAGCTGGTGGTGGTGGGCACATGCTGTAGTTCAGCTAC	3384	PR	14-AUG-2000;	2000US-0225758.
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AC	ABAI9112;					
XX	23-JAN-2002 (first entry)					
DT	Human nervous system related polynucleotide SEQ ID NO 11443.					
DE	Human; nontropic; neuroprotective; cytostatic; dermatological; virucide;					
XX	Immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;					
KW	antiparkinsonian; antischlicking; antianaemic; antiarthritic; cancer;					
KW	antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;					
KW	antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;					
KW	antiparasitic; cardiac; immune disorder; cardiovascular disorder;					
KW	neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.					
OS	Homo sapiens.					
XX	WO200159063-A2.					
PN	16-AUG-2001.					
XX	17-JAN-2001; 2001WO-US01334.					
PF	31-JAN-2000; 2000US-0179065.					
XX	04-FEB-2000; 2000US-0180628.					
PR	24-FEB-2000; 2000US-0184664.					
PR	02-MAR-2000; 2000US-0186350.					
PR	16-MAR-2000; 2000US-0189874.					
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PR	19-MAY-2000; 2000US-0205515.					
PR	07-JUN-2000; 2000US-0209467.					
PR	28-JUN-2000; 2000US-0214886.					
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PR	11-JUL-2000; 2000US-0217487.					
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PR	14-AUG-2000; 2000US-0224519.					
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PR	05-DEC-2000;	2000US-0251030.
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PR	05-JAN-2001;	2001US-0259678.
XX	(HUMA*) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX		
DD	WPI; 2001-541565/60.	
XX		
PT	Nucleic acids encoding 3224 human nervous system antigen polypeptides,	
PT	useful for preventing, diagnosing and/or treating nervous system	
PT	cancers and metastases -	
XX		
PS	Disclosure; SEQ ID NO 11443; 1701pp + Sequence Listing; English.	
XX		
CC	The invention relates to novel genes (ABA11004-ABA21534) and proteins	
CC	(ABA14678-ABA18001) useful for preventing, treating or ameliorating	
CC	medical conditions e.g. by protein or gene therapy. The genes are	
CC	isolated from a range of human tissues disclosed in the specification.	
CC	The nucleic acids, proteins, antibodies and (ant)agonists are useful	
CC	in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast	
CC	and ovarian cancer and other cancers of the adrenal gland, bone, bone	
CC	marrow, breast, gastrointestinal tract, liver, lung, or urogenital;	
CC	(b) immune disorders e.g. Addison's disease, allergies, autoimmune	
CC	hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's	
CC	disease, multiple sclerosis, rheumatoid arthritis and ulcerative	
CC	colitis; (c) cardiovascular disorders such as myocardial ischaemias;	
CC	(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and	
CC	epilepsy; and (f) infectious diseases such as viral, bacterial, fungal	
CC	and parasitic infections.	
CC	Note: The sequence data for this patent did not form part of the	
CC	printed specification, but was obtained in electronic format directly	
CC	from WFO at ftp.wipo.int/pub/published_pct_sequences.	

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Db	11220	TCGGGAGGCTGAGATACGAGAACACTTGNACCAGAGGTTGGAGATTGTCAGTGAGCCAA	11161
Qy	3445	GACCACACCACTCGCTCCAGCTGGGCGCACAGAGTAGACACCTGTTTCTTAAGAAGAACA	3504
Db	11160	GAAGCGCCCACTGCACCTCCAGCCTGGCGCAAGAGTGAGACTGTGTCTCAAAAAAAA	11101
Qy	3505	AAGAAAAAA 3513	
Db	11100	CAAAAGCAA 11092	
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XX	AC	ABQ87681;	
XX	CC	(first entry)	
DT	18-SEP-2002	Human oestrogen receptor alpha gene.	
DE	XX	Human; oestrogen; receptor; oestrogen receptor alpha; cytostatic;	
XX	XX	osteopathic; cardiant; cancer; osteoporosis; cardiovascular disorder;	
KW	KW	chromosome 6q25.1; gene; ds.	
KW	XX	Homo sapiens.	
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FT FT      7.3%; Score 317.4; DB 24; Length 465237;

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Best Local Similarity 93.5%; Pred. No. 3.5e-50;
Matches 330; Conservative 1; Mismatches 22; Indels 0; Gaps 0;

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QY 2447 GCATTTGGAGGCGGCGGCTGGATCATGAGTFCAGGAGATCGAGACCATCTGGCT 2506
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RESULT 14
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ID ABA90193 standard; DNA; 465237 BP.
XX AC ABA90193;
XX DT 11-FEB-2002 (first entry)
XX DE Human oestrogen receptor alpha gene.
XX KW Human: oestrogen receptor alpha; ESR-alpha; ER; chromosome 6; Syne-2;
XX KW synaptic nuclei expressed gene 2; haplotype; cytostatic; osteopathic;
XX KW cardiant; vasotropic; gene therapy; vaccine; cancer; osteoporosis;
XX KW cardiovascular disease; oestrogen receptor; ds.
XX OS Homo sapiens.
XX PN WO200162969-A2.
XX PD 30-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US05358.
XX PR 22-FEB-2000; 2000US-183756P.
XX PR 20-OCT-2000; 2000US-0692414.
XX PR 24-JAN-2001; 2001US-0768184.
XX PA (PEKE ) PE CORP NY.
XX PI Kalush F, Cassel MJ, Hwang SS, Winn-Deen ES;
XX DR WPI; 2002-041152/05.
XX DR P-PSDB; AAG68251.
XX PT Novel variant of estrogen receptor alpha polypeptide useful for
XX PT determining the biological activity of a protein for high throughput
XX PT screening and for raising antibodies that elicit an immune response in
XX PT host -
XX PS Example; Fig 1 page 1-93; 333pp; English.
XX CC The present invention describes an isolated peptide (I) consisting of an
XX CC amino acid sequence selected from: (a) the amino acid sequence of a
XX CC variant of the oestrogen receptor alpha (ESR-alpha) protein in AAG68251;
XX CC or (b) a fragment comprising at least 10 contiguous amino acids of the

```


Db 46192 TGACATCATAGGCTGG---GCATGGTGGCTCACACCTGTAACTCTAACACTCTGGGAGGC 46248
Qy 3253 CAAGGCGAGGAGCATCATCTTGAAGCCAGAAATTCAAGACCACCTGGTCAACATTGTAAAGA 3312
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34	262.8	6.1	1988	4	US-08-367-841A-11
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ALIGNMENTS

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; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Krommal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/724,394A
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20

Query Match 7.7%; Score 336.4; DB 2; Length 246240;
Best Local Similarity 59.8%; Pred. No. 7.9e-65;
Matches 680; Conservative 1; Mismatches 432; Indels 25; Gaps 6;

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QY 2446 AGCACTTTGGAGCGCGGGTGGATCATGAGTCCAGGATCGAGACCATCTCGGC 2505
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QY 2506 TAACAAGGTGAACCCCGCTCTCTACTAAAAATACAAAAATTAGCGCGCGGTGGCGG 2565
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QY 2566 GCGCCTGTAGTCCAGCTTCTCGGAGGCTGAGGAGGAGTGGGTGAACCCGGGAGG 2625
Db 107235 GCGCCTGTGGTCCAGCTACTCGGAGGTTGAGGAGGAGTGGGTGAATCCGGGAGG 107294

QY 2626 CGAGCTTGCAGTGCAGCAAGTTCGCCACTGCAGTCCGAGTCCGCGCTGGCGGACAG 2685
Db 107295 CGAGGTTGCAGTGCAGCGAGATTGCGCACT- - - - -GCATTCCAGCCTGGGCGACAG 107347

QY 2686 AGCGAGCTCTGTYTCAAAAAAATAAAAAAATAAAAAAATAAATAGGAAACGCA 2745
Db 107348 AGCAAGCTCGTCTCAGAAAAAATAAAAAAATAAAAAATAGTAAAGAGAAAAA 107407

QY 2746 TCTTTACACTTAGGTTTGGTTCGTCTATCTATAAAAAAGGGTTGGATTAAGTATCC 2805
Db 107408 TGCAATTTGCTTTGGGACTTTTAAATATTTAGTCTACAAATCTAGCCACCATAGAAATCTGC 107467

QY 2806 CTGGCACTTATAAATGTAGGCTTAATATTAATCATAGATCGAGGATAGTTCAATCT 2865
Db 107468 TGATTAATACGGGTTCTGTTAAATGGAACATGCAATTTGGGGGAAAAAAGAGGAGT 107527

QY 2865 TAGTCGCTCTCTAGTCTCTCTCTATACCAATCTGAGCAATTTTACAATTTAGAAA 2925
Db 107528 GTTTTAGTGATTTGTTTTTACACTCTTTATATAAATAATTTAAGCAATCTTGAGGG 107587

QY 2926 GACAAATAACTCGTGGGTAGTCTAGTATATAAATACCAAGAAAAATATTTAGAGG 2985
Db 107588 AATATTTATTTCTACTTGTAACTGCATAAAGTTATGAGATAAAGTTACAAGCTATATCA 107647

QY 2985 AATTAAGTTGAACACATG- - -TTAACAAATCTACCAAGTGG- -GATTTGCCCTGTGAT 3042
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QY 3043 TAAAGATGCTGTAACATTTGGCGCAGTAGTTATTAATTTGAAAAATGTTTATAGCCAATA 3102
Db 107708 GAAATGTCATAAATACATTAAGATATATTTTATAAACCAATTCAGAAGGCAATA 107767

QY 3103 TATAATTTTATTAATAATACAGTTTCATCAGTCA- - - - -TTAGTATTTCAATTA 3155
Db 107768 CCCAATTTCAAAATCATATTAATTTGAAAAATTAATTAGGCGAGCAAAATATTTCTGGAAT 107827

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QY 3216 AAAGGCTGTGTGCACTGCTCACACCTGTGGGAGCCCAAGGAGGATCATCTTGGAGG 3275
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QY 3276 CCAGAAGTTCAAGACCAACCTGGTCAACATTTGTAAGCCCTGTCTCTACAAAAAATA 3335
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RESULT 2
US-08-724-394A-21
; Sequence 21, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
; US-08-724-394A-21

Query Match 7.7%; Score 336.4; DB 2; Length 246240;
Best Local Similarity 59.8%; Pred. No. 7.9e-65;
Matches 680; Conservative 1; Mismatches 432; Indels 25; Gaps 6;

QY 2386 TTCCTTTTCATCTAAAAAATAAAACCATAGCGCGCGGTGGCTACGCGCTGTAAATCCC 2445
Db 107055 TTATATTTTCTTTGGATAAAGTCAGTAGCGGGCGGTGCTATGCTGTGATCCT 107114

QY 2446 AGCACTTTGGAGCGCGGGTGGATCATGAGTTCAGGATCGAGACCATCTCGGC 2505
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Db 107235 GCGCCTGTGGTCCAGCTACTCGGAGGTTGAGGAGGAGTGGGTGAATCCGGGAGG 107294

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QY 2686 AGCGAGCTCTGTYTCAAAAAAATAAAAAAATAAAAAAATAAATAGGAAACGCA 2745
Db 107348 AGCAAGCTCGTCTCAGAAAAAATAAAAAAATAAAAAATAGTAAAGAGAAAAA 107407

QY 2746 TCTTTACACTTAGGTTTGGTTCGTCTATCTATAAAAAAGGGTTGGATTAAGTATCC 2805
Db 107408 TGCAATTTGCTTTGGGACTTTTAAATATTTAGTCTACAAATCTAGCCACCATAGAAATCTGC 107467

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QY 2926 GACAAATAACTCGTGGGTAGTCTAGTATATAAATACCAAGAAAAATATTTAGAGG 2985
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QY 3043 TAAAGATGCTGTAACATTTGGCGCAGTAGTTATTAATTTGAAAAATGTTTATAGCCAATA 3102
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QY 2806 CTGGCACTTATAAATGTTAGGCTTAAATATTATTCATAGATCGAGGATAGTTTCACTT 2865
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QY 2926 GACAAATAACTGGTGGGTTACTGTAGTATATTAATACCAAGAAAAATTAATTTAGAAG 2985
Db 107588 AACATTTTATCTTACTGTAACTGCATAAAGTTATGAGATAAAGTTACAAGCTATATCA 107647
QY 2986 AATTAAGTTTCAAAACCATG--TTAACAAATCTACCAAGTGG-GATTGCTGTGAT 3042
Db 107648 CATACAGTTGTAGCTTTATAATATTAATATGAATTTCTACAGATAAATATGCTAATATGAT 107707
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US-09-128-155-17
; Sequence 17 Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)-(176373)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17
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Query Match 7.2%; Score 310.8; DB 3; Length 176373;
Best Local Similarity 62.4%; Pred. No. 3.3e-59;
Matches 703; Conservative 1; Mismatches 348; Indels 74; Gaps 11;
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US-09-813-817-3

; Sequence 3, Application US/09813817

; Patent No. 6340583

; GENERAL INFORMATION:

; APPLICANT: YAN, Chunhua et al.

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL0011178

; CURRENT APPLICATION NUMBER: US/09/813,817

; CURRENT FILING DATE: 2001-03-22

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows version 4.0

; SEQ ID NO 3

; LENGTH: 59065

; TYPE: DNA

; ORGANISM: Human

US-09-813-817-3

Query Match 6.7%; Score 289.6; DB 4; Length 59065;

Best Local Similarity 58.6%; Pred. No. 1.2e-54;

Matches 693; Conservative 1; Mismatches 410; Indels 78; Gaps 8;

QY 2397 TAAAAAATAAACCATAGGCGGCGGCTGACGCTGTAATCCCGACACTTTGGG 2456

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Db	15244	CCTCA-----CAGTATTACTGTGAATAAAGTGTGTGTAGCACATGGGAACACTATTTCACAG	15299
QY	3079	TTTGGAAAAATGTTTATAGCCAATATATAATTTTATTTTAAATATACAGTTTTCATCAGTC	3138
Db	15300	AGCACTCATGAATGTTTGTCTTTGTTTATTAGTATTCTAGAGAGGCAATGTCTGCCAGGG	15359
QY	3139	TATTAGTATTTCATTAAGTCTAAGATGCCATCAGTGGTGTAGCAAAACCACTGTTTATTG	3198
Db	15360	CTGAATAATATGTGTGAATTTGGTGAATTTGTCGCACATATCTAAAGAAGTAGTTATTTTTT	15419
QY	3199	CACATGC-----TAAGAAAGAATAAAGGGCTGTGTGCAGTGGCTCACACCTG----	3244
Db	15420	CAATTAAACTTAGTTTAAAAACCAATATRAGCGGAGCGCAGTGGCTCACACCTGTAAAT	15479
QY	3245	-----TGGAGCCCAAGGAGGAGGAGCATCACTTTGAGGCCAGAAGTTCAAGACCAAC	3294
Db	15480	CCCAGCACTTTGGGAGGCCGAGGTGGCGAGATCATTTTGTAGTTCAGAGATTCGAGACTAGC	15539
QY	3295	CTGCTCAACATTTGAACACCCCTGTCTCTACAAAAAATAAAAAAGTT-----AAAAATTAGC	3349
Db	15540	CTGCCAACATATGTTGAACCCCTGTCTCTCTAAAAAAAATAAAAAAGTACAAAAATTAGC	15599
QY	3350	TGGTGGCGGTGGCCACATGCTCTAGTTTCCAGCTACTCTGGAGGCTAAGGTGGGAGGATTG	3409
Db	15600	CAGCATGATGGCAGGTCCCTGTAATCCAGCTACTTTGGGAGCGCGAGGAGAGAATTG	15659
QY	3410	CTAGAGCCACGGTGTGGAGCTGCAATGAGCTGTGACCACACCACTGCGCTCAGCGTG	3469
Db	15660	CTTGAACCCAGAGGAGGTGGAGGTTGTAGTGAGCCGAGTTTGTGCCACTGCACTTTCAGCCTG	15719
QY	3470	GGCAACAGAGTGAGACCCCTGTTTCTTAAAGAAAGAAAGAAAAA	3511
Db	15720	GTCACAGAGGAGACACTGTCTCAAAAAAATAAAAAA	15761
RESULT 10			
US-09-978-197-3			
; Sequence 3, Application US/09978197			
; Patent No. 6403353			
; GENERAL INFORMATION:			
; APPLICANT: YAN, Chunhua et al.			
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC			
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES			
; TITLE OF INVENTION: THEREOF			
; FILE REFERENCE: CL001178DIV			
; CURRENT APPLICATION NUMBER: US/09/978,197			
; CURRENT FILING DATE: 2001-10-17			
; PRIOR APPLICATION NUMBER: 09/813,817			
; PRIOR FILING DATE: 2001-03-22			
; NUMBER OF SEQ ID NOS: 4			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 3			
; LENGTH: 59065			
; TYPE: DNA			
; ORGANISM: Human			
US-09-978-197-3			
Query Match 6.7%; Score 289.6; DB 4; Length 59065;			
Best Local Similarity 58.6%; Pred. No. 1.2e-54;			
Matches 693; Conservative 1; Mismatches 410; Indels 78; Gaps 8;			
QY	2397	TAAAAATAAAACCATAGGCGCGGGTGGCTCAGCGCTGTAAATCCAGCACTTTGGG	2456
Db	14591	TAAAAAATAATGGAGGCGCAGCAGCGGTGGCTCAGCGCATGTAAATCCAGCACTTTGGG	14650
QY	2457	AGGCGGAGGGGGTGGATCATAGTCCAGGAGATCGAGACCATCTCGCTAACCAAGTGA	2516
Db	14651	AGGCGGAGGGGGGGGATCACAGGTCCAGGATTCGAGACCATCTCGCTAACCAAGTGA	14710
QY	2517	AACCCCGCTCTCTACTAAAAATACAAAAATPAGCCGGCGCGGTGGGGGGCGCTGTAGT	2576

[illegible]

RESULT 11

QY 3194 TTATGCACTGCTAAGAAAGATAAAGGCT-GTGTGCACTGGCTCACACCTG----- 3244
Db 4737 GTATTCAAGGTGGTAAAGAAATCCAGTGGGTGCACTGGCTCACGCTGTATCCCA 4796
QY 3245 -----TGGAGCCAGCCAGGACATCACTTGAGGCCAGAGTTCAAGACCACTGG 3298
Db 4797 GTACTTTGGAGGCTGAGCCAGGAGCGCTTGAGCTCAGAGTTCAAGACCACTGA 4856
QY 3299 TCAACATTTAAGACCTGCTCTACAAAAAAGTTAAAAATTAGCTGGTGCGG 3358
Db 4857 GCACATAGTAGACCTCATCTACTAAAAAATAAATACCGCATGTAGCAT 4916
QY 3359 TGGCAGATG-----CTGTAGTCCAGCTACTCTGGAGGCTAAGTGGGAGGATG 3409
Db 4917 GTGCCTGTAGTCCAGCTACTCTAGTCCAGCTACTTGGAGGCTGAGGTGAGAGGATCA 4976
QY 3410 CTAGACCCAGCTGTGGAGCTGCAATGAGCTGTGACCAACCACTGCTCCAGCGTG 3469
Db 4977 CTGAGCCAGGAGATCGAGGCTGAGTGAGCCATATACGCCACTGCATCCAGCCTG 5036
QY 3470 GGCAACAGAGTGGACCTGTTTCTTAAAGAAAGAAAGAAA 3510
Db 5037 GGCACTAAGCAAGCCCTGTCTCAAAAAATTTTAAAAAA 5077

RESULT 12
PCT-US94-04496-63
; Sequence 63, Application PC/TUS9404496
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Macklewitz &
; ADDRESSEE: Norris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca Esq., Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1242
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8342 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2...265
; FEATURE:
; NAME/KEY: CDS

; LOCATION: 595...666
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2353...2484
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3032...3145
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6788...6934
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7967...8062
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 8304...8342
; PCT-US94-04496-63

Query Match 6.6%; Score 288.6; DB 5; Length 8342;
Best Local Similarity 57.8%; Pred. No. 9.8e-55;
Matches 648; Conservative 1; Mismatches 430; Indels 42; Gaps 6;

QY 2415 GCCGGCGCGTGTCTACCGCTGTAAATCCAGCAGCTTTGGGAGCGCGGCTGGAT 2474
Db 3974 GCTGGGCACGGTGCCTCACGCTGTAAATCCAGCAGCTTTGGGAGCGCGGAT 4033
QY 2475 CATGAGTCAGGAGATCGAGACCATCTCGCTAACAGGTGAACCCCGTCTCTATAA 2534
Db 4034 CACAAGGTCAGGAGATCCAGACCATCTCGCTAACAGGTGAACCCCGTCTCTATAA 4093
QY 2535 AATAC-AAAAAATTAGCCGGCGGCTGGCGGCGCTGTAGTCCAGCTTCTCGGAGG 2593
Db 4094 AATACAAAAAATTAGCCGGCGGCTGTGGCGGCGCTGTAGTCCAGCTTCTCGGAGG 4153
QY 2594 CTGAGGAGGAGATGCGGTGAACCCGGGAGCGGAGCTTGCAGTGAGCCCAAGATTGCGC 2653
Db 4154 CTGAGGAGGAGATGCGGTGAACCCGGGAGCGGAGCTTGCAGTGAGCCCAAGATTGCGC 4213
QY 2654 CACTGCAGTCCGAGTCCGCGCTGGGCGGAGCAGAGAGCTGTGTCAAAAAAATAA 2713
Db 4214 CACT-----GCAGTCCGCGCTGGGCGGAGCAGAGAGCTGTGTCAAAAAAATAA 4266
QY 2714 AAAAAAACCATAAATAGAGAAACCATCTTTACACTTAGGCTTTGAGTTCTGT 2773
Db 4267 AAGTGTAGGCGATATATAATGCCAAATATGAAGTCTTAA------GATAATATAT 4316
QY 2774 ATCTATAAAAAAGGTTTGGATTAAAGTGAATGATCCCTGGCAGCTTATAAATGTTAGGCTTAA 2833
Db 4317 ATTAATATTAGTGTGGTCCAAAGTAAATTCAGTAAATGAGGAGATGTCATG 4376
QY 2834 TATTATCATAGATCGAGGATAGTTTTCATTTAGTCCGCTCTTACTGCTTCTCTAT 2893
Db 4377 ACATATCACTGAGTGAAGAGAGGATTAAGATAATATAAAGCAACATCCCATCTT 4436
QY 2894 ACCAATCTGAGACCATTTTACAATTTAGAAAGACAAATACCTGTTGGGTACTTGATA 2953
Db 4437 AGTTTGAAGAGTGTGTTTAAAGTATATATCTAGAAACCAATCTGGAAGGATTCACACCA 4496
QY 2954 GTATAATAACCAAGAAATTAATTTTGAAGGAATTAAGTTTGAAGACCATGTGTAACA 3013
Db 4497 AATATTAAGAGTGTGTTGATTTAGGACCTTTATTTGTTCTCTGTTTTTTTT 4556
QY 3014 ATTCTACCAAGTGGGATTTGCGCTGTGATTAAGATGCTGTAAACATTTGGGCGAGTAGT 3073
Db 4557 TTTTAACTTTCTGAGTTTTTTGGAGTATGTACCACTTTTACATGAGGAGGAAAAAGT 4616
QY 3074 TATTAATTGAAGATTTTATAGCCAAATATATAATTTTTTATTTAATATACAGTTTCAT 3133
Db 4617 AGCAAAATTTTAAATAGGAGCAGTAGTTTGTCAATTTATAGGAGCATATCTTACATCCT 4676
QY 3134 CAGTCTATTAGTATTTCATTAAGTCAAGATGCCATGAGTGGTGTAGCAAAACACCTGTT 3193
Db 4677 TTACAGTTCTTAATCTCTGCGAGATACCTCTTTTGGCTTTATTACTTACCACATAGATAT 4736

QY 3194 TTATGCACTGCTAAGAAAGATAAAGGCT-GTGTGAGTGGCTCACAGCTG----- 3244
 DB 4737 GTATTCAAAGGTGTTAAGAAATCCAGTGGTGCAGTGGCTGTAATCCCA 4796
 QY 3245 -----TGGGACGCCAGGAGGAGCATCTAGAGCCAGAAAGTTCAAGACCAAGCTGG 3298
 DB 4797 GTACTTTGGGAGGCTGACGAGGAGGAGCCGCTTGAGCTCAGGAGTTCAAGACCAAGCTGA 4856
 QY 3299 TCAACATTGTAAGACCTGCTCTACAAAAAAGTTAAATAGCTGGGTGGG 3358
 DB 4857 GCACCATAGTAGACCTCACTCTACTTAAATAAATAAATAAATACAGGATGGTAGCAT 4916
 QY 3359 TGGCAGATGC-----CTGTAGTCCAGCTACTCTGAGGCTGAAGGTGGGAGGATMG 3409
 DB 4917 GTGCTGTAGTCCAGCTACTCTAGTCCAGCTACTTGGGAGGCTGAGGTGAGAGATCA 4976
 QY 3410 CTAGAGCCAGGCTGTGGAAGCTGCAATGAGCTGTGACCAACACCTGGCTCCAGCGTG 3469
 DB 4977 CTTGAGCCAGGAGATCGAGGCTGCAGTGCAGCCATTATACGCCATTCACCTCCAGCCTG 5036
 QY 3470 GGCAACAGATGAGACCTGTTCTTAAAGAAAGAAAGAA 3510
 DB 5037 GGCAACTAAGCAAGACCTGTCTCAAAAAAATTTTAAAAA 5077

RESULT 13
 US-08-080-255-6
 ; Sequence 6, Application US/08080255
 ; Patent No. 5487970
 ; GENERAL INFORMATION:
 ; APPLICANT: Rowley, Janet D.
 ; APPLICANT: Diaz, Manuel O.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 ; TITLE OF INVENTION: DETECTING GENE REARRANGEMENTS AND
 ; TITLE OF INVENTION: TRANSLOCATIONS
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P. O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: USA
 ; ZIP: 77210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/080,255
 ; FILING DATE: 19930617
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parker, David L.
 ; REGISTRATION NUMBER: 32,165
 ; REFERENCE/DOCKET NUMBER: ARCD:072/PAR
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (512) 320-7200
 ; TELEFAX: (512) 474-7577
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8392 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-080-255-6

Query Match 6.6%; Score 288.6; DB 1; Length 8392;
 Best Local Similarity 57.8%; Pred. No. 9.8e-55;
 Matches 648; Conservative 1; Mismatches 430; Indels 42; Gaps 6;

QY 2415 GCCGGCGCGGTGGCTCACGCCTGTAATCCAGCACTTTTGGAGCGCGAGCGGTGGAT 2474
 DB 4025 GCTGGCAGCGGTGCTCACGCCTGTAATCCAGCACTTTTGGAGCGCGAGCGGAT 4084
 QY 2475 CATGAGGTGAGGAGATGAGAGCAATCTGCTGAACAGGTGAACCCCGCTCTACTATA 2534
 DB 4085 CACAGGTGAGGAGATGAGAGCAATCTGCTGAACAGGTGAACCCCGCTCTACTATA 4144
 QY 2535 AATAC-AAAAAATFAGCGCGCGGTGGCGCGCTGAGTCCAGCTTCTCGCGGAGG 2593
 DB 4145 AATACAAAAAATFAGCGCGGTGGCGCGCTGAGTCCAGCTTCTCGCGGAGG 4204
 QY 2594 CTGAGGCGAGGAGATGCGGTGAACCCGGGAGCGGAGCTTTCAGTGAGCCAAATGCGC 2653
 DB 4205 CTGAGGCGAGGAGATGCGGTGAACCCGGGAGCTTTCAGTGAGCCAAATGCGC 4264
 QY 2654 CACTGCAGTCCGCGAGTCCGCGCTGGCGCAGAGCACTCTGTTCAAAAAATAA 2713
 DB 4265 CACT-----GCACTCCGCGCTGGCTACAGAGCAGACTCCGCTCTCAAAAAAATAA 4317
 QY 2714 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2773
 DB 4318 AAGTGTAGGCATATATAATGCGCAATATGAAGTCCCTAAA-----GATAATATAT 4367
 QY 2774 ATCTATAAATAAAGGTTTGGATTAAAGTATCCCTGGCAGCTTATAAATAAATAA 2833
 DB 4368 ATTAATATTATTAGTGGTGCAGAAAGTAAATTCAGAGTAATATGAAGATGTCATG 4427
 QY 2834 TATTATTATAGATCGAGGATGTTTCATTCTTAGTGCCTCCTTAGTCACTCTTCTAT 2893
 DB 4428 ACATATCACTGAGTGAAGAGCAGGTTACAAGATAATATAAAGCACAATCCCATCT 4487
 QY 2894 ACCAATCTGAGACCATTTTACAATTTAGAAAAAGACAAATTAACCTGTTGTTGATA 2953
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 QY 2954 GTATAATAACCAAGAAAAATAAATTTAGAGGAATTAAGTTTGAACCAACATGTTAAACA 3013
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 QY 3134 CAGTCTATTAGTATTTCATTAAAGTCTTAAGATGCCATCAGTGGTTAGCAACACCACTGT 3193
 DB 4728 TTACAGTTCTTTAAATTTCTGCGAGATACCTCTTTGGCTTATTACTTACCACATAAGAT 4787
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 DB 4788 GTATTCAAAGGTGTTAAGAAATCCAGTGGTGCAGTGGCTCAGCTGTAAATCCCA 4847
 QY 3245 -----TGGGACGCCAGGAGGAGCATCTTGAAGCCAGAGAGTTCAGCAACCACTGG 3298
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 QY 3470 GGCAACAGATGAGACCTGTTCTTAAAGAAAGAAAGAA 3510

; ZIP: 77210
 ; COMPUTER READABLE FORM:
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 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/05857
 ; FILING DATE: 19930617
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 07/900,689
 ; FILING DATE: 17/06/92
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parker, David L.
 ; REGISTRATION NUMBER: 32,165
 ; REFERENCE/DOCKET NUMBER: ARCD:072/PAR
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (512) 320-7200
 ; TELEFAX: (512) 474-7577
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8392 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; PCT-US93-05857-6

Query Match 6.68; Score 288.6; DB 5; Length 8392;
 Best Local Similarity 57.8%; Pred. No. 9.8e-55;
 Matches 648; Conservative 1; Mismatches 430; Indels 42; Gaps 6;
 QY 2415 GCGGGCGCGGTGCTACGCTGTAATCCAGCACATTTGGAGGCGGAGCGGGTGGAT 2474
 DB 4025 GCTGGGACGGTGGCTACGCTGTAATCCAGCACATTTGGAGGCGGAGCGGGTGGAT 4084
 QY 2475 CATGAGGTGAGGAGATCGAGACCATCTCTGCTAAACAGGTGAACCCCGCTCTACTAAA 2534
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 QY 2535 AATAC-AAAAAATTAGCGGGCGGGTGGAGGCGGAGGCGGCTAGTCCAGCTTCTCGGAGG 2593
 DB 4145 AATACAAAAAATTAGCGGGTGGTGGGCGGCGGCTAGTCCAGCTACTCGAGAGG 4204
 QY 2594 CTGAGGCGAGGAGATGGCGTGAACCGGAGGCGGAGGCTTGCAGTGAGCCAAAGATTGCGC 2653
 DB 4205 CTGAGGCGAGGAGGAGGATGAACCGGAGGCGGAGGCTTGCAGTGAGCCGAGATCGCC 4264
 QY 2654 CACTGAGTCCGCGAGTCCGCGCTGGGCGACAGAGGAGACTCTGTTCAAAAAAATAA 2713
 DB 4265 CACT-----GCATCCCGCTGGGTACAGCAAGAGCTCCGCTCAAAAAAATAA 4317
 QY 2714 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2773
 DB 4318 AAGTGTAGGCGATATATAATGCAAAATATGAAGTCTCTCAAAAAAATAAATAAATAA 4367
 QY 2774 ATCTATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2833
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 DB 4548 AATATTAAAGAGTGGGTGGATTATGGTGACCTTTATTTGTTTCTCTGCTGTTTTTTTT 4607

QY 3014 ATTCTACCAAGTGGGATTTGCTGTGATTAAAGATGCTGTAAACATTTTGGCCAGTACT 3073
 DB 4608 TTTTAACTTTCTGAGTTTTCGAGTAUGTACCACCTTTACATAGGAAGAAAAAGT 4667
 QY 3074 TATAATTTGAAAAATGTTTATAGCCCAATATATAATTTTATTTAATAATATACAGTTTCAT 3133
 DB 4668 AGCACAATTTTAAATAGGAAGCAGTAGTTTGTCAATTTATAAGGACATATCTCTACATCT 4727
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 DB 4728 TTACAGTCTTAAATTCCTGGCAGATACCTCTTTTGGCTTATTACTTACCACATAGATAT 4787
 QY 3194 TTATGCACTGCTAAGAAAGAAATAAAGGCT-GTGTGAGTGGCTCACACTG----- 3244
 DB 4788 GTATTCAAAGGTGTTAAAGAAATCCAGTCCGGTGCAGTGGCTCAGCTGTAAATCCCA 4847
 QY 3245 -----TGGACGCCCAAGGCGAGGAGCATCATTGAGGCCAGAGTTTCAAGACCAACTGG 3298
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 QY 3410 CTAGAGCCAGGTTGTTGGAAGCTGCAATGAGCTGTGACCAACCACTGCGCTCCAGCGTG 3469
 DB 5028 CTTGAGCCAGGAGATCGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 5087
 QY 3470 GGCAACAGAGTGAAGACCTGTTTCTTAAAGAAAGAAAGAA 3510
 DB 5088 GGCAACTAAGCAAGACCTGCTCTCAAAAAAATAAATAAATAA 5128

Search completed: February 28, 2003, 09:48:00
 Job time : 3326 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 09:06:17 ; Search time 268 Seconds
(without alignments)
10105.882 Million cell updates/sec

Title: US-09-730-559B-7

Perfect score: 4343

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 460893 seqs, 311809382 residues

Total number of hits satisfying chosen parameters: 921786

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	877.2	20.2	3770	9	US-09-924-396B-19
3	345.8	8.0	16511	10	US-09-764-869-2064
4	317.4	7.3	465237	10	US-09-933-267A-1
5	311.8	7.2	368004	10	US-09-949-654-3
6	311	7.2	20210	10	US-09-764-870-598
7	310.8	7.2	176373	9	US-10-095-407-17
8	310.2	7.1	172637	9	US-09-805-458A-3
9	309.6	7.1	13873	9	US-09-764-868-1282
10	309.2	7.1	27007	9	US-09-764-868-1424
11	309	7.1	152331	9	US-10-095-407-16
12	307	7.1	110096	10	US-09-880-107-1542
13	306.4	7.1	2275	10	US-09-764-864-209
14	305.6	7.0	31730	10	US-09-764-877-3810
15	305.4	7.0	326014	10	US-09-731-231A-3
16	305.2	7.0	1503841	9	US-09-946-807-1
17	305.2	7.0	1503841	10	US-09-795-668-1
18	305.2	7.0	1503841	10	US-09-795-686-1
19	304.2	7.0	180557	12	US-10-003-806-6

c 20	304.2	7.0	180557	12	US-10-003-806-9	Sequence 9, Appli
c 21	302.6	7.0	4205	10	US-09-764-869-1884	Sequence 1884, Ap
c 22	301.6	6.9	327	10	US-09-764-877-2571	Sequence 2571, Ap
c 23	300.4	6.9	15643	10	US-09-764-870-638	Sequence 638, App
c 24	300.4	6.9	31314	10	US-09-764-877-3875	Sequence 3875, Ap
c 25	299.2	6.9	18000	10	US-09-800-631-17	Sequence 17, Appl
c 26	296	6.8	106323	10	US-09-803-661-3	Sequence 3, Appli
c 27	294.6	6.8	3083	10	US-09-764-869-1703	Sequence 1703, Ap
c 28	291.6	6.7	145831	10	US-09-969-708-79	Sequence 79, Appl
c 29	291.6	6.7	145831	10	US-09-954-456-2116	Sequence 2116, Ap
c 30	291.2	6.7	36159	12	US-10-135-687-3	Sequence 3, Appli
c 31	290.8	6.7	6892	10	US-09-764-869-1720	Sequence 1720, Ap
c 32	290	6.7	684973	10	US-09-263-959-1	Sequence 1, Appli
c 33	289	6.7	46050	10	US-09-820-003A-3	Sequence 3, Appli
c 34	288.4	6.6	40645	9	US-10-216-441-3	Sequence 3, Appli
c 35	288.4	6.6	40645	10	US-09-818-656A-3	Sequence 3, Appli
c 36	288.2	6.6	32183	10	US-09-764-869-1494	Sequence 1494, Ap
c 37	287.6	6.6	57130	10	US-09-835-081-3	Sequence 3, Appli
c 38	286.8	6.6	5251	10	US-09-764-869-1431	Sequence 1431, Ap
c 39	286.2	6.6	2550	10	US-09-880-107-2131	Sequence 2131, Ap
c 40	286.2	6.6	5095	10	US-09-824-637-3	Sequence 3, Appli
c 41	285	6.6	17509	10	US-09-880-107-2097	Sequence 2097, Ap
c 42	282.6	6.5	174424	10	US-09-967-768A-314	Sequence 314, App
c 43	282	6.5	27332	10	US-09-764-847-1555	Sequence 1555, Ap
c 44	281	6.5	32204	10	US-09-764-855-327	Sequence 327, App
c 45	280.8	6.5	34641	10	US-09-954-456-1110	Sequence 1110, Ap

ALIGNMENTS

RESULT 1
US-09-924-396B-17
; Sequence 17, Application US/09924396B
; Patent No. US20020165349A1
; GENERAL INFORMATION:
; APPLICANT: Kirsch, Wolff
; APPLICANT: Lennart, Anton
; APPLICANT: Kelln, Wayne
; APPLICANT: Kang, Dae-Kyung
; APPLICANT: Levine, Rodney
; APPLICANT: Rouault, Tracey
; TITLE OF INVENTION: IRON-REGULATING PROTEIN-2 (IRP-2) IS
; FILE REFERENCE: LOMAU.140A
; CURRENT APPLICATION NUMBER: US/09/924.396B
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/222,863
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 2867
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-924-396B-17

Query Match 22.8%; Score 990; DB 9; Length 2867;
Best Local Similarity 100.0%; Pred. No. 8.3e-169;
Matches 990; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	34	TACCTTATTGAACATTAAATGACAGTTTCACATAGAAGTTCTTCGATGTATCTAAACTT	93
Db	1	TACCTTATTGAACATTAAATGACAGTTTCACATAGAAGTTCTTCGATGTATCTAAACTT	60
QY	94	GGCACCACCAAGTATGATGTTCTGCCTTACTCAATACGGGCTCTTGTGGAGCTGCTGTACGA	153
Db	61	GGCACCACCAAGTATGATGTTCTGCCTTACTCAATACGGGCTCTTGTGGAGCTGCTGTACGA	120
QY	154	AATTGTGATGGCTTTTAAATGAAGAAGGAGATGTTATGAACATTTTACAGCTGGAACACC	213
Db	121	AATTGTGATGGCTTTTAAATGAAGAAGGAGATGTTATGAACATTTTACAGCTGGAACACC	180


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QY 898 GAAACAGAGCAGTTATGCTGTGTCGCCAGTTTCTCTTACTTACACGAGGTGGTGA 957
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 912 GAGACAGGCGAGTTATGCTGTGCGCTGCCAGTTACTTACTTTACACGAGGTGGTGA 971

QY 958 TGTGAGTTAACTGGTGCATCAAAACCCCTTTTGTACATCCATAGATGTTCTTGTGTA 1017
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 972 TGTGAGCTAACTGGTGCATCAATGCTTTTGTACATCCATAGATATTTGCTAGGCATT 1031

QY 1018 ACAAAG 1023
  ||| |||
Db 1032 ACAAAG 1037

RESULT 3
US-09-764-869-2064
; Sequence 2064, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2064
; LENGTH: 16511
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (14362)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-869-2064

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Query Match      8.0%; Score 345.8; DB 10; Length 16511;
Best Local Similarity 61.3%; Pred. No. 4.1e-53;
Matches 682; Conservative 1; Mismatches 408; Indels 22; Gaps 7;

QY 2404 TAAACACATAGCGCGCGCGTGCCTGACCCCTGTAATCCAGCAGCTTTGGGAGCGCA 2463
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 645 TTAATAAAAGAGCGCGGTGGTGGTGCCTACACCTGTAATCCAGCAGCTTTGGGAGCGCTA 704

QY 2464 GCGGGTGGATCATGAGTTCAGGATCGAGACCATCTGCTAACAAAGGTGAACCCCG 2523
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 705 GCGGGCAGATCAGGAGTCAAGATCAAAACCATCTGGCTAACACGCTGAACCCCG 764

QY 2524 TCTCTACTAAATAACAAA--AAATTAGCGCGCGCGTGGCGCGCTGTAGTCCAG 2581
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 765 TCTCTACTAAATAACAAAATAATAGCCAGGATGTTGGTGGCAGCTGTAGTCCAG 824

QY 2582 CTTCTCGGAGGCTGAGCAGGAGAAATGGCGTGAACCCGCGGAGCGGAGCTTCAGTGAG 2641
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 825 CTACTCGGAGCTGAGCAGGAGAAATGGCGTGAACCCGAGGAGCAGCTTCAGTGAG 884

QY 2642 CCAAGATTCGCGCATGCGAGTCCGAGTCCGCGCTGGCGGACAGAGCAGACTCTGYTC 2701
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 885 CCAAGATTCGCGCATGCGAGTCCGAGTCCGCGCTGGCGGACAGAGCAGACTCTGYTC 937

QY 2702 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2761
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 938 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 997

QY 2762 TTGATTTCTGTATCTATAAAAAAGGT--TTGGATTAAAGTATCCCTGGCAGCTATATA 2819
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 998 GAGAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1057

QY 2820 ATGTTAGGCTTAATATTTATCATAGATCGAGGATAGTTTCAATCTTAGTCGCTCCTTA 2879
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1058 CAATAAACATGAAAAAATAATTTTCAGAAATATCAAAAAAAGTACAAATGAAACATTTA 1117

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QY 2880 GTCACTCTTCTATACCAATCTGAGACCATTTTACAAATTTAGAAAAAGACAAATAGTGT 2939
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1118 GATAGTTTCTATCTATACCAAAATGAAAGCATATCAAAAAATAGTAACTGGTCAAAATG 1177

QY 2940 TGGTTTCTTCTATAGTATAATAACCAAGAAAAATAATTTTAGAAGGAATTAAGTTTGA 2999
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1178 AGAGAGACTGTCACTGGAAGTCTCAATTTGTTTACCGTTTCTAGACAAATGAGCAGTTCT 1237

QY 3000 CCACATGTTAAACAAATCTACCAAGTGGGATTTGCTGTGATTAAGATGCTGTGAACA 3059
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1238 ATTAGTTTATTAAGAAAGTCCATGATCTTATCTGTGACCTATCTACTATTTCCTCT 1296

QY 3060 TTTGGGCGAGTAGTTATAATTTGAAAAATCTTATAGCAATATATAATAATTTTATTTAA 3119
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1297 TTTCTTGACTTTAATTCAAACTCCCAAAATGTTTGAAGTTCATGCTGCGAGCTATGTGA 1356

QY 3120 ATATACAGTTTCACTATTAATTAAGTATTAATTAAGTTCATAGTCAAGATGCCATCAGTGT 3179
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1357 GTATGAATATTGACTAACTAATTTGTAAGTTGAGATGCTATGAGAATA----TGGGGA 1412

QY 3180 CAACACACCTGTTTATGCACTGCTAAGAAAGAAATAAAGGCTGTGTCAGTGGCTCAC 3239
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1413 AATTTGACATTTCTTAAAGTATTAATTAAGTCAAGACAGCAGTGGTTTACGCTGTAATCCC 1472

QY 3240 ACCTGTGGGAGCCCAAGGAGGAGCATCTCTGAGGCCAGAGTTCAAGACCAACCTGTGT 3299
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1473 CACTTTGGGAGGCCAAGATGGAGGAGTCACTTGGAGGCCAGAGTTTCAAGAACTACCTGG 1532

QY 3300 CAACATGTTAGACCCCTCTCTACAAAAAATAAAGTTTAAAAATAGTGGTGGTGGT 3359
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1533 CAACATAGTGAGA--CCTGTCTCAACAAAAAGTAAA-----AAAAATTAATGATTGGT 1586

QY 3360 GGCACATGCTGTAGTCTTCCAGTCTCTGAGGAGTAAAGTGGGAGGATTTCTAGAGCCAC 3419
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1587 GGTGATGCTGTGTGCTCCAGTCTTGGAGGCTGAGGAGTGGTGGAGGATGCTTTGAGACTA 1646

QY 3420 GGTGTTGGAAGTCAATGAGTGTGACACACAGTCCGCTCCAGGTTGGGCAACAGAG 3479
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1647 GGAGATCAAGCTGAGTGTGATCATGCCACTGCACTGCAGCTCCAGCTGGGCAACAGAA 1706

QY 3480 TGAGACCTGTTTCTTAAAGAAAGAAAGAAAAA 3512
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1707 TGAGACCTTCTCTAATAATAATAATAATA 1739

RESULT 4
US-09-933-267A-1/c
; Sequence 1, Application US/09933267A
; Patent No. US20020123095A1
; GENERAL INFORMATION:
; APPLICANT: Kalush, Francis et al.
; TITLE OF INVENTION: Estrogen receptor alpha variants and
; FILE REFERENCE: CL000258C14
; CURRENT APPLICATION NUMBER: US/09/933,267A
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/160626
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 60/183756
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 09/692414
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/768184
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 09/804076
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 09/826314
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 465237
; TYPE: DNA

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; ORGANISM: human
US-09-933-267A-1

Query Match      7.3%; Score 317.4; DB 10; Length 465237;
Best Local Similarity 93.5%; Pred. No. 1.1e-47;
Matches 330; Conservative 1; Mismatches 22; Indels 0; Gaps 0;

QY 2387 TCTTTTCATCCCTAAAAATAAAACCATAGCGCGGCGCGGTGGCTCAGCCCTGTAATCCCA 2446
DB 47735 TATTTCTCTTAAGGACAAAGAGCGCAGTGGCGGCGCGGTGGCTCAGCCCTGTAATCCCA 47676
QY 2447 GCACCTTTGGGAGGCGGAGCGGGTGGATCATGAGGTTCAGGAGATCGAGACCATCTCGCT 2506
DB 47675 GCACCTTTGGGAGGCGGAGCGGGTGGATCATGAGGTTCAGGAGATCGAGACCATCTCGCT 47616
QY 2507 AACAGGTGAACCCCGTCTCTACTATAAATAACAAAAATAGCCGGCGCGGTGGCGGG 2566
DB 47615 AACAGGTGAACCCCGTCTCTACTATAAATAACAAAAATAGCCGGCGCGGTGGCGGG 47556
QY 2567 CGCCTGTAGTCCCGAGCTTCTCGGAGGCTGAGCGAGAGATGCGTGAACCCGGGAGGC 2626
DB 47555 CGCCTGTAGTCCCGAGCTTCTCGGAGGCTGAGCGAGAGATGCGTGAACCCGGGAGGC 47496
QY 2627 GGAGCTTGCAGTGAAGCAAGATTGGCCACTGCAGTCCGCGAGTCCGGCCTGGCGCAGCA 2686
DB 47495 GGAGCTTGCAGTGAAGCAAGATTGGCCACTGCAGTCCGCGAGTCCGGCCTGGCGCAGCA 47436
QY 2687 GCGAGACTCTGTYTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 2739
DB 47435 GCGAGACTCCGCTCTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 47383

RESULT 5
US-09-949-654-3/c
; Sequence 3, Application US/09949654
; Patent No. US20020127644A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000817
; CURRENT APPLICATION NUMBER: US/09/949,654
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 60/231,572
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 368004
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(368004)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-654-3

Query Match      7.2%; Score 311.8; DB 10; Length 368004;
Best Local Similarity 90.7%; Pred. No. 1e-46;
Matches 331; Conservative 1; Mismatches 33; Indels 0; Gaps 0;

QY 2370 AATATCTAATCTGTGTTCTTTCATCTCAAAAAATAAAACCATAGCGCGGCGGTGGC 2429
DB 286574 AGTGTTTCTTATTTTGTGGGAATAAATATGTAGCAATAGCGCGGCGGTGGC 286515
QY 2430 TCACGCGCTTAATCCAGACATTTGGGAGCGGAGCGGGTGGATCATGAGTTCAGGAGA 2489
DB 286514 TCACGCGCTTAATCCAGACATTTGGGAGCGGAGCGGGTGGATCATGAGTTCAGGAGA 286455
QY 2490 TCGAGACCATCTGGGTACACAGGTGAACCCCGTCTCTACTAAAAATAACAAAAATTAG 2549
DB 286454 TCGAGACCATCTGGGTACACAGGTGAACCCCGTCTCTACTAAAAATAACAAAAATTAG 286395
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QY 2550 CCGGGCGCGGTGGCGGCGCCTGTAGTCCAGCTTCTCGGGAGGTGAGGCAGGAGAATG 2609
DB 286394 CCGGGCGCGGTGGCGGCGCCTGTAGTCCAGCTTCTCGGGAGGTGAGGCAGGAGAATG 286335
QY 2610 GGGTGAACCCGGGAGGCGGAGCTTGCAGTGAAGCCAGATTGGCCACTTGCAGTCCGAGT 2669
DB 286334 GGGTGAACCCGGGAGGCGGAGCTTGCAGTGAAGCCAGATTGGCCACTTGCAGTCCGAGT 286275
QY 2670 CCGGCTGTGGCGACAGAGAGAGACTCTGTYTCAAAAAAATAAAAAAATAAAAAAATAAAAA 2729
DB 286274 CCAGCCTGTGGCGACAGAGCGAGACTCCGTCTCAAAAAAATAAAAAAATAAAAAATATGTAGCA 286215
QY 2730 TAAAT 2734
DB 286214 ATAAAT 286210

RESULT 6
US-09-764-870-598/c
; Sequence 598, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 598
; LENGTH: 20210
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-870-598

Query Match      7.2%; Score 311; DB 10; Length 20210;
Best Local Similarity 88.9%; Pred. No. 7.5e-47;
Matches 335; Conservative 1; Mismatches 41; Indels 0; Gaps 0;

QY 2392 CATCCTAAAAATAAAACCATAGCGCGGCGGTGGCTCAGCCCTGTAATCCAGCACT 2451
DB 16817 CATGCATGAAAAAGTCCCGAGACGCGCGGCGGTGGCTCAGCCCTGTAATCCAGCACT 16758
QY 2452 TTGGGAGCGGAGCGGGTGGATCATGAGTCAGAGATCGAGACCATCTTGGCTAACAA 2511
DB 16757 TTGGGAGCGGAGCGGGTGGATCATGAGTCAGAGATCGAGACCATCTTGGCTAACAA 16698
QY 2512 GGTGAAACCCCGTCTCTACTATAAATAACAAAAATAGCGGCGCGGTGGCGGGCGCCT 2571
DB 16697 GGTGAAACCCCGTCTCTACTATAAATAACAAAAATAGCGGCGCGGTGGCGGGCGCCT 16638
QY 2572 GTAGTCCAGCTTCTCGGAGGCTGAGGCAGAGATGGGTGAACCCGGGAGCGGAGC 2631
DB 16637 GTAGTCCAGCTTCTCGGAGGCTGAGGCAGAGATGGGTGAACCCGGGAGCGGAGC 16578
QY 2632 TTGCAGTGAGCAAGATTGCGCCACTGCGAGTCGCGCTCGGCTCGGCGACAGAGCGAG 2691
DB 16577 TTGCAGTGAGCCGAGATTGCGCCACTGCGAGTCGCGCTCGGCTCGGCGACAGAGCGAG 16518
QY 2692 ACTCTGTYTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAATCTTTA 2751
DB 16517 ACTCCGTCTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAATATGACAGCGCTTG 16458
QY 2752 CACTTAGGTTTGAGTT 2768
DB 16457 CATGTTACCTTTGAGCT 16441

RESULT 7
US-10-095-407-17
; Sequence 17, Application US/10095407
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; Patent No. US20020164330A1
; GENERAL INFORMATION:
; APPLICANT: Pao, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/032001
; CURRENT APPLICATION NUMBER: US/10/095,407
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/091,650
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/054,646
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
US-10-095-407-17

Query Match      7.2%; Score 310.8; DB 9; Length 176373;
Best Local Similarity 62.4%; Pred. No. 1.3e-46;
Matches 703; Conservative 1; Mismatches 348; Indels 74; Gaps 11;

Qy 2397 TAAAAATAAACCAATAGCGCGCGGGTGGCTCAGCGCTGAATCCCGACACTTTGGG 2456
      ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64735 TAAAAATGCCACTCTTTGGCGGCGCGGTGGCTCAGCGCTGAATCCCGACACTTTGGG 64794

Qy 2457 AGGCGGAGCGGGTGGATCATGAGTTCAGGATCAGAGATCAGACCATCTTGGCTAACAGGTGA 2516
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64795 AGGCGGAGCGGGTGGATCATGAGTTCAGGATCAGGATCAGAGATCAGACCATCTTGGCTAACAGGTGA 64854

Qy 2517 AACCCCGTCTCTACTAAAAATACAAAAAATAGCCGGCGCGGTGGCGCGCGCTTACTGT 2576
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64855 AACCCCGTCTCTACTAAAAATACAAAAAATAGCCGGCGCGGTGGCGCGCGCTTACTGT 64914

Qy 2577 CCCAGCTTCTCGGAGGCTGAGGAGGAGATGGCGTGAACCCGGGAGCGGAGCTTGA 2636
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64915 CCCAGCTTCTCGGAGGCTGAGGAGGAGATGGCGTGAACCCGGGAGCGGAGCTTGA 64974

Qy 2637 GTGAGCCAAAGATTCGCGCACTGCAGTCCCGAGTCCGCGCTGGCGGAGAGAGACTCT 2696
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64975 GTGAGCCAGATTCGCGCACTGCAGTCCCGAGTCCGCGCTGGCGGAGAGAGACTCC 65034

Qy 2697 GTTTCAAAAAATAAAAAAATAAAAAAATAAAATAGAGAAACCGCATCTTTACACTT 2756
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65035 GTTTCAAAAAATAAAAAAATAAAAAAATAAAATAGAGAAACCGCATCTTTACACTT 2816

Qy 2757 AGGGTTTCTGAGTTCTGTATCTATAAAAAAGGGTTTGATTAACTGATCCCTGGCACTTAT 2816
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65092 GGGGAAGGAGGATAGAAATGCAAAAGTGAACGACCACTCAGGAGGTGAGGCAAT 65151

Qy 2817 AAATGTTAGGCTTAATATTAATTCATAGATCAGGATAGTTCATCTTAGTGGCTCC 2876
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65152 GGAAGTGTGAGGAGAGACTGACATCTTAGACTCGGGCAA-----TAGGAGAGAAG 65201

Qy 2877 TTATGCTCTTCTCTATACCAATCTGAGACCATTTTACAATTTAGAAAAAGACAAATAACT 2936
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65202 GTGGTGAGGAT-----ATATCTGGGCATAAAGGCAACAGACTAGCT 65245

Qy 2937 GTTGGGTTACTTGATAGTATAATAACCAAGAAATAATTTTAGAGGAATTAAGTTTGG 2996
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65246 GATGGCGT-----CAAGCTAGGAGATGAGGAAAGAAATAATCAAGG 65290

Qy 2997 AAACACATGTTAAACAAATCTACCAAGTGGGATTTGGCTGTGATTAAAGATGCTGTA 3056
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65291 CATTCATAGGTTTGGGGTTGAGTGAAGTGGGATAT-----TTACAGAAATGGAGAG 65344

Qy 3057 ACAATTGGGCGAGTAGTTATAAATTTGAAAAATGTTTATAGCCAAATATATAATTTTATT 3116
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 65345 TCTGGGAAGGGCAAGTATTTGGGGCAGGGTCAAAAGTTCTGTATTTTGGCCAAGT 65404
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3117 TAAATATACAGTTTCATCAGCTCTATTAGTATTTCAATTAAGTCTTAAGATGCCATCAGTGT 3176
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65405 TAATTAATATTTGAGATACCTCT-----TAGGTGTCCAAGTGAAGATGTCAAAACAGTCAA 65459
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3177 TAGCAAAACACCACTGTTTATGCACTGCTAAGAAAGAAATAAAGGGCTGTGTGCAGTGGCT 3236
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Db 65511 CAGCACTTTGGAGGCTGAGGTGAGAGATCACTTGGAGCCAGGAGTTTGTGATCAGCT 65570
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Qy 3297 GGTCAACATTTGAAGACCTGTCTC--TACAAAAAATAAAAGTTAAATATAGCTGGT 3354
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Db 65571 GGGCAATAGAGCAAGACCCCTGTCTCCACACACACACACACAAAAAGTCTCCAGGC 65630
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Qy 3355 GCGGTGGCAGATGCTCTAGTTCAGCTACTTGGAGGCTTAAGTGGGAGGATTTGCTAGA 3414
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Db 65631 ATGTGGCAGATGCTCTAGTCCAGCTACTCAGGAAGCTGAGGCAGGAGGATCACTTGA 65690
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Qy 3415 GCCACGGTGTGGAGCTGCAATGAGCTGACCACTG-----ACTGGCTCCAGG 3467
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Db 65691 GCC--CATGTTCAAGGCTGAGTGAGCTAATCACTACTCAATACACTACACTCCAGCC 65749
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Qy 3468 TGGCAACAGAGTGAGACCTGTTTCTTAAAGAAAGAAAGAAAAA 3513
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Db 65750 TGGATGACAGAGAGACCTCAUATTATTAATAATAAATTTAAAAA 65795
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RESULT 8
US-09-805-458A-3/c
; Sequence 3, Application US/09805458A
; Patent No. US20020042100A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al
; TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000722
; CURRENT APPLICATION NUMBER: US/09/805,458A
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 172637
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(172637)
; OTHER INFORMATION: n = A,T,C or G
US-09-805-458A-3

Query Match      7.1%; Score 310.2; DB 10; Length 172637;
Best Local Similarity 95.5%; Pred. No. 1.7e-46;
Matches 318; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

Qy 2394 TCCTAAAAATAAAACCATAGCGCGCGGTGGCTTCAGCGCTGTAATCCCGAGCACTTT 2453
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Db 15207 TCTTTAAAAATAACAGTTGGCCAGCGCGGTGGCTCAGCGCTGTAAATCCCGAGCACTTT 15148

Qy 2454 GGGAGCGCGAGCGGGTGGATCATGAGTCAGGATCGAGACCATCTCGGTGTAACAAG 2513
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Db 15147 GGGAGCGCGAGCGGGTGGATCATGAGTCAGGATCGAGACCATCTCGGTGTAACAAG 15088

Qy 2514 TGAACCCCGCTCTACTATAAAATACAAAAATTAGCCGCGCGGTGGCGGCGCTGT 2573
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Db 15087 TGAACCCCGCTCTCTACTATAAAATACAAAAATTAGCCGCGCGGTGGCGGCGCTGT 15028

Qy 2574 AGTCCCAAGCTTCTCGGGAGGCTGAGCAGGAGAAATGCGCTGAACCCCGGAGCGAGCTT 2633
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; CURRENT APPLICATION NUMBER: US/09/731,231A
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 326014
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(326014)
; OTHER INFORMATION: n = A,T,C or G
US-09-731-231A-3

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Query Match	7.08;	Score 305.4;	DB 10;	Length 326014;
Best Local Similarity	93.3%;	Pred. No. 1.4e-45;		
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QY 2453	TGGGAGGCCGAGGCGGGTGGATCATGAGTTCAGGAGATCGAGACCATCCTGGCTAAACAAG	2512		
Db 248365	TGGGAGGCCGAGGCGGGTGGATCATCGAGGTCAGGAGATCGAGACCATCCTGGCTAAACAAG	248306		
QY 2513	GTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCGGGCGCGGTGGCGGGCGGCTG	2572		
Db 248305	GTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCGAGCGCGGTGGCGGGCGGCTG	248246		
QY 2573	TAGTCCCGAGCTTCTCGGGAGGCTCGAGCGAGAGATGCGTGAACCCGGAGGCGGAGCT	2632		
Db 248245	TAGTCCCGAGCTTCTCGGGAGGCTCGAGCGAGAGATGCGTGAACCCGGAGGCGGAGCT	248186		
QY 2633	TGCAGTCAGCCCAAGATTGCGCCACTTGCAGTCCGCGCTTGGCGGACAGAGCCGAGA	2692		
Db 248185	TGCAGTCAGCCGAGATTGCGCCACTTGCAGTCCGCGCTTGGCGGACAGAGCCGAGA	248126		
QY 2693	ETCTGTTTCAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA	2733		
Db 248125	CTCGTCTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA	248085		

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Job time : 3791 secs

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Run on: February 28, 2003, 05:39:35 ; Search time 8804 seconds
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4341.8	100.0	4343	29	US-09-730-559B-7 Sequence 7, Appl
2	3248.4	74.8	62724	68	US-60-243-468-591 Sequence 591, App
3	3248.4	74.8	62724	68	US-60-243-742-99 Sequence 99, Appl
4	1023	23.6	3280	25	US-09-654-935A-257 Sequence 257, App
5	1023	23.6	3290	1	PCT-US01-08656-4031 Sequence 4031, Ap
6	1023	23.6	4684	17	US-09-359-922-8303 Sequence 8303, Ap
7	1023	23.6	4684	17	US-09-359-922-8303 Sequence 8303, Ap
8	1023	23.6	4684	34	US-09-919-002-8303 Sequence 8303, Ap
9	1019.8	23.5	4194	18	US-09-471-275-1719 Sequence 1719, Ap
10	1019.8	23.5	4194	18	US-09-496-914A-7145 Sequence 7145, Ap
11	1019.8	23.5	4194	22	US-09-560-875A-7145 Sequence 7145, Ap
12	1019.8	23.5	4729	76	US-60-324-185-26664 Sequence 26664, A
13	1019.8	23.5	4729	76	US-60-339-453-290 Sequence 290, App
14	1004	23.1	5034	77	US-60-339-453-63 Sequence 63, Appl
15	990	22.8	2867	34	US-09-924-396B-17 Sequence 17, Appl
16	990	22.8	2867	66	US-60-222-863-17 Sequence 17, Appl
17	990	22.8	3558	16	US-09-205-070-12807 Sequence 12807, A
18	990	22.8	3558	17	US-09-340-623-12807 Sequence 12807, A
19	990	22.8	3558	33	US-09-898-888-12807 Sequence 12807, A
20	990	22.8	3558	33	US-09-898-888A-12807 Sequence 12807, A
21	877.2	20.2	3770	34	US-09-924-396B-19 Sequence 19, Appl

22	877.2	20.2	3770	66	US-60-222-863-19	Sequence 19, Appl
23	767.8	17.7	814	29	US-09-736-119-1624	Sequence 1624, Ap
24	654.8	15.1	5601	80	US-60-360-207-5266	Sequence 5266, Ap
25	526.2	12.1	605	30	US-09-760-475-125	Sequence 125, App
26	526.2	12.1	605	30	US-09-760-475-1331	Sequence 1331, Ap
27	506.6	11.7	561	24	US-09-637-889-4744	Sequence 4744, Ap
28	504	11.6	597	29	US-09-736-119-350	Sequence 350, App
c	29	494.4	581	1	PCT-US02-25766-12391	Sequence 12391, A
30	469.6	10.8	608	30	US-09-785-276A-56174	Sequence 56174, A
31	435.8	10.0	508	65	US-60-213-362-6374	Sequence 6374, A
32	435.8	10.0	508	76	US-60-324-185-27788	Sequence 27788, A
33	381	8.8	391	32	US-09-834-366-37869	Sequence 37869, A
34	381	8.8	391	63	US-60-197-873-37869	Sequence 37869, A
35	381	8.8	414	19	US-09-528-409-111255	Sequence 111255,
36	381	8.8	414	35	US-09-933-524-111255	Sequence 111255,
37	381	8.8	414	35	US-09-933-524A-111255	Sequence 111255,
38	377.2	8.7	440	18	US-09-489-036-34205	Sequence 34205, A
39	377.2	8.7	440	35	US-09-943-143-34205	Sequence 34205, A
40	372	8.6	409	35	US-09-528-409-49242	Sequence 49242, A
41	372	8.6	409	35	US-09-933-524-49242	Sequence 49242, A
42	372	8.6	409	35	US-09-933-524A-49242	Sequence 49242, A
43	369	8.5	407	19	US-09-528-409-49241	Sequence 49241, A
44	369	8.5	407	35	US-09-933-524-49241	Sequence 49241, A
45	369	8.5	407	35	US-09-933-524A-49241	Sequence 49241, A

ALIGNMENTS

RESULT 1
US-09-730-559B-7
; Sequence 7, Application US/09730559B
; GENERAL INFORMATION:
; APPLICANT: ISHIWATA, TETSUYOSHI
; APPLICANT: SAKURADA, MIKIO
; APPLICANT: KAWABATA, AYAKO
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: NISHI, TATSUNARI
; APPLICANT: KUGA, TETSURO
; APPLICANT: SAWADA, SHIGEMASA
; APPLICANT: TAKEI, MASAMI
; APPLICANT: SHIBATA, KENJI
; APPLICANT: FURUYA, AKIKO
; TITLE OF INVENTION: Iga NEPHROPATHY-ASSOCIATED GENE
; FILE REFERENCE: 766.21 CIP
; CURRENT APPLICATION NUMBER: US/09/730,559B
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 4343
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1029)
US-09-730-559B-7

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Best Local Similarity	100.0%;	Pred. No. 0;		
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Qy	1	ATGGACGCCCAAGCAGGATACGCCCTTTGAGTACCTTATGAAACATTAAATGACAGT	60	
Db	1	ATGGACGCCCAAGCAGGATACGCCCTTTGAGTACCTTATGAAACATTAAATGACAGT	60	
Qy	61	TCACATAGAAGTCTTCGATGTATCTAAACCTTGGCACCAGATGATGTCTGCCCTTAC	120	
Db	61	TCACATAGAAGTCTTCGATGTATCTAAACCTTGGCACCAGATGATGTCTGCCCTTAC	120	
Qy	121	TCAATACGGGCTCTGTTGGAAGCTGCTGACGAAATGTGATGGCTTTTAAATGAAGAAG	180	
Db	121	TCAATACGGGCTCTGTTGGAAGCTGCTGACGAAATGTGATGGCTTTTAAATGAAGAAG	180	

Qy	181	GAAGATGTTATGAACATTTTAGACTTGGAAACCAAAACCAAGCAATGTTGAAGTGCCCTTT	240	
Db	181	GAAGATGTTATGAACATTTTAGACTTGGAAACCAAAACCAAGCAATGTTGAAGTGCCCTTT	240	
Qy	241	TTCCCTCCCGTGTCTTCTTCAAGATTTTACATGGAATACCAAGATGGTGGATTTTGCT	300	
Db	241	TTCCCTCCCGTGTCTTCTTCAAGATTTTACATGGAATACCAAGATGGTGGATTTTGCT	300	
Qy	301	GCATAGAGGAGCAGTGAACACTCTTGGAGCTCATCCTCAGAAAGCTCCATCGCTTGT	360	
Db	301	GCATAGAGGAGCAGTGAACACTCTTGGAGCTCATCCTCAGAAAGCTCCATCGCTTGT	360	
Qy	361	CCGACAGATCTTACAGTTGACCAATCTTTACAAATGACTTTCAGTAAATGTCGAATACAG	420	
Db	361	CCGACAGATCTTACAGTTGACCAATCTTTACAAATGACTTTCAGTAAATGTCGAATACAG	420	
Qy	421	ANTGCACCAATCTTGGAGTGTGACTGCAGAAAGCAGGAAGCTCTCTCCACTTAA	480	
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Qy	481	GTGAGCTTAAGAGCTTCCCTGCAGAGCCAGACTACCTGCGGAGGATCTTGTGATCT	540	
Db	481	GTGAGCTTAAGAGCTTCCCTGCAGAGCCAGACTACCTGCGGAGGATCTTGTGATCT	540	
Qy	541	GGAGAACTAGCGCGAAACTCAGGAACATTTTCTTCGAGATTGAGAATACACCCATCTG	600	
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Db	601	TGTCCTTTTCATTTGCAACAGTGCCTGAACCTGAAACAGTGTAAAAATCAAGAAGTA	660	
Qy	661	GAATTCGGCAGAAATCGAGAGAGCTTCAGTTTTTAAAGTGGAGTTCAAGAGTTTTAAAG	720	
Db	661	GAATTCGGCAGAAATCGAGAGAGCTTCAGTTTTTAAAGTGGAGTTCAAGAGTTTTAAAG	720	
Qy	721	AATGTGSCAGTGATCCCTCCTGGAAGTGGAAATGGCTCATCAATAAATAGATAATTTG	780	
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Qy	781	TCAAGAGTGGTTTTTGAAGAAAAGACCTCCCTCCAGACAGTGTAGTCGCGACAGAT	840	
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Qy	841	TCACACATACAGTGTGAATGTTTAGGATTCCTGGGTGGGGGTTCGAGGCAATTGAA	900	
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Qy	901	ACAGAAGCAGTTATGCTTGGCTGSCAGTTTCTCTTACTTTACCAGAGTGGTTGGATGT	960	
Db	901	ACAGAAGCAGTTATGCTTGGCTGSCAGTTTCTCTTACTTTACCAGAGTGGTTGGATGT	960	
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Db	1021	AAGCTAAGTTAAAGTTGTTAGTCTTATGACTTACTGAACATTTATTTATATAAAATG	1080	
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Qy	1141	AGCCACATCATAGTTATCATAGTAATAACAAACAAACAGAGCATTTAGTTGTACTTAA	1200	
Db	1141	AGCCACATCATAGTTATCATAGTAATAACAAACAAACAGAGCATTTAGTTGTACTTAA	1200	
Qy	1201	TAAATACAAAGAAATTTGTTGTTTTCACCTTATGTTAGCTCATTTAGTCTCTTATAACAGC	1260	
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Qy	1261	CTGTGAGATGGATACATATTACTATTCTCATTTGTAAGTCTGAGAAAACTAAGGTACAGTAG	1320
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Qy	1321	GGTTTACTGACTTACCAAAAGGTCGAAAGCCGTGAGTAATAGGGCTAGAGCAAGATTCCA	1380
Db	1321	GGTTTACTGACTTACCAAAAGGTCGAAAGCCGTGAGTAATAGGGGTAGAGCAAGATTCCA	1380
Qy	1381	GGCAGTCAGATTCTTGAGTCATGCTTAACCATTAATGCGCTATTAGTGCCTTGTGGCCTTA	1440
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Qy	1921	CTTCTCGATACCTCAGTGAAGAAATGATAATGCCCTCCCTCTCAGCATTTGGTATTGA	1980
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Db	1981	TCCTTCTCCCTAATTTAGAAAAAGATTTGGCAATCTTAGAGAAATTAATGATCAACGTAT	2040
Qy	2041	GATACCAAAAGATCAAGTAGTAATTTGGGAATTCAGAGATTATTTCTTAGAGGAAAAGGAG	2100
Db	2041	GATACCAAAAGATCAAGTAGTAATTTGGGAATTCAGAGATTATTTCTTAGAGGAAAAGGAG	2100
Qy	2101	TATCCCATATATGTTTTTACAGAAATCAATCTTTTACTTTAGACATCTCTGAAAACTAAACGC	2160
Db	2101	TATCCCATATATGTTTTTACAGAAATCAATCTTTTACTTTAGACATCTCTGAAAACTAAACGC	2160
Qy	2161	TGCTTTTTAGCCCTCTAGCTGTTTTTTCCTGCAATATTACTGTGTTTTTTTGACAT	2220
Db	2161	TGCTTTTTAGCCCTCTAGCTGTTTTTTCCTGCAATATTACTGTGTTTTTTTGACAT	2220
Qy	2221	TTTAGTTTTAATGTTAAAAAATTAATCTATATATATGTTTTACATTTATTTGAATATTGA	2280
Db	2221	TTTAGTTTTAATGTTAAAAAATTAATCTATATATATGTTTTACATTTATTTGAATATTGA	2280
Qy	2281	TTACTTCTTTTTTGGAGATCCGTCCCATTTGATGTCCTTATAGGAATAAATCCCTGATTGT	2340
Db	2281	TTACTTCTTTTTTGGAGATCCGTCCCATTTGATGTCCTTATAGGAATAAATCCCTGATTGT	2340
Qy	2341	TTTTTTTGATGAGACGACATTTTGGTTGTGTAATATCTAACTGTGTTTTCTTTCATCCCTAAA	2400

Db	2341	 TTTTTTCATGAGACGACATTTGGTTGTGAATATCTAATCTGTCTTTTCATCCTAAA	2400
Qy	2401	AAATAAAACCATAGCGCGCGGTGCTCAGCCTCTAATCCACGACTTTGGGAGGC	2460
Db	2401	AAATAAAACCATAGCGCGCGCGGTGCTCAGCCTCTAATCCACGACTTTGGGAGGC	2460
Qy	2461	CGAGCGGGTGGATCATGAGGTGAGAGATCGAGACCCTCTGGCTAACAGGTGAACCC	2520
Db	2461	CGAGCGGGTGGATCATGAGGTGAGAGATCGAGACCCTCTGGCTAACAGGTGAACCC	2520
Qy	2521	CCGTCTCTACTAAAAATACAAAAAATTAGCCGGCGCGGTGGCGGGCGCTGTAGTCCCA	2580
Db	2521	CCGTCTCTACTAAAAATACAAAAAATTAGCCGGCGCGGTGGCGGGCGCTGTAGTCCCA	2580
Qy	2581	GCTTCTCGGAGGCTGAGCGAGAGAAATGGCGTGAACCCGGAGCGGAGCTTGCAGTGA	2640
Db	2581	GCTTCTCGGAGGCTGAGCGAGAGAAATGGCGTGAACCCGGAGCGGAGCTTGCAGTGA	2640
Qy	2641	GCCAAGATTGCGCCACTGCGAGTCCGCGCTCGGCGTGGCGACAGCGAGACTCTGTYT	2700
Db	2641	GCCAAGATTGCGCCACTGCGAGTCCGCGCTCGGCGTGGCGACAGCGAGACTCTGTYT	2700
Qy	2701	CAAAAAAATAAAAAAATAAAAAACCAATAAATGAGGAAACGCATCTTTACACTTAGGG	2760
Db	2701	CAAAAAAATAAAAAAATAAAAAACCAATAAATGAGGAAACGCATCTTTACACTTAGGG	2760
Qy	2761	TTTGAGTTCTCTGATCTATAAAAAAGGTTTCGATTAGTTCAGTCCCTGGCACTTATAAAA	2820
Db	2761	TTTGAGTTCTCTGATCTATAAAAAAGGTTTCGATTAGTTCAGTCCCTGGCACTTATAAAA	2820
Qy	2821	TGTTAGGGCTTAATATATTTCATAGATCAGAGATAGTTTCATCTTAGTCGCCCTCCCTAG	2880
Db	2821	TGTTAGGGCTTAATATATTTCATAGATCAGAGATAGTTTCATCTTAGTCGCCCTCCCTAG	2880
Qy	2881	TCACCTCTCTCATACCAATCTGAGACCATTTTACAAATTTAGAAAAGACAAATAACTGGTT	2940
Db	2881	TCACCTCTCTCATACCAATCTGAGACCATTTTACAAATTTAGAAAAGACAAATAACTGGTT	2940
Qy	2941	GGGTTACTTCATAGTATATAACCAAGAAAATAATTTTACAGGAATATAGTTTGAAC	3000
Db	2941	GGGTTACTTCATAGTATATAACCAAGAAAATAATTTTACAGGAATATAGTTTGAAC	3000
Qy	3001	CACATGTTAAACAATCTACCAAGTGGGATTTGGCTGTGATTTAAAGATGCTGTAAACAT	3060
Db	3001	CACATGTTAAACAATCTACCAAGTGGGATTTGGCTGTGATTTAAAGATGCTGTAAACAT	3060
Qy	3061	TTGGGCCAGTAGTTATAATTTGAAAATGTTTATAGCCAAATATAATTTTTTTATTTAAA	3120
Db	3061	TTGGGCCAGTAGTTATAATTTGAAAATGTTTATAGCCAAATATAATTTTTTTATTTAAA	3120
Qy	3121	TATACAGTTTCATCAGTCTATTAGTATTTCATTAGTCTAAGATGCCATCAGTGGTTAGC	3180
Db	3121	TATACAGTTTCATCAGTCTATTAGTATTTCATTAGTCTAAGATGCCATCAGTGGTTAGC	3180
Qy	3181	AAACACCACCTGTTTTATGCACTGCTAAGAAAACAATAAAGGCTGTGTGCACTGGCTCACA	3240
Db	3181	AAACACCACCTGTTTTATGCACTGCTAAGAAAACAATAAAGGCTGTGTGCACTGGCTCACA	3240
Qy	3241	CCTGTGGACGCCAAGCGAGGACATCCTTTGAGCCCAAGAGTTTCAAGACCAACCTGGTC	3300
Db	3241	CCTGTGGACGCCAAGCGAGGACATCCTTTGAGCCCAAGAGTTTCAAGACCAACCTGGTC	3300
Qy	3301	AACATTGTAGACCCCTGCTCTACAAAAAATAAAGTTAAAAATTAGCTGGTGGCGGTG	3360
Db	3301	AACATTGTAGACCCCTGCTCTACAAAAAATAAAGTTAAAAATTAGCTGGTGGCGGTG	3360
Qy	3361	GCACATGCCCTGATGTTCCAGCTACTCTGGAGGCTAAGGTGGGAGGATTTGCTAGAGCCACG	3420
Db	3361	GCACATGCCCTGATGTTCCAGCTACTCTGGAGGCTAAGGTGGGAGGATTTGCTAGAGCCACG	3420
Qy	3421	GTGTTGGAAGCTGCAATGAGCTGTGACCAACACCACTCGGCTCCAGCGTGGGCAACAGAGT	3480

QY 1707 CACTGAGCTTTTAAAGCATATTAATACACAGGCTCAGGATTTCCCTAGTGAAACAATAATT 1766
DDB 36895 CACTGAGCTTGTAAAGCATATTAATACACAGGCTCAGGATTTCCCTAGTGAAACAATAATT 36954
QY 1767 TGTAACTCTCTCTCCTAAATGTCTGGCCTTGTGTAACCTTTATTTTAAATGATTAAATCCCTA 1826
DDB 36955 TGTAACTCTCTCTCCTAAATGTCTGGCCTTGTGTAACCTTTATTTTAAATGATTAAATCCCTA 37014
QY 1827 TTTTGTAAATGAATGATGACCTGGAATAATTTCCACATATATAATTTCCCAATTTGAGTCCCAAT 1886
DDB 37015 TTTTGTAAATGAATGATGACCTGGAATAATTTCCACATATATAATTTCCCAATTTGAGTCCCAAT 37074
QY 1887 CTCAGCAATTTTGGTTAGATTAATGTTACGAAGGCTTTCTCGGATCTCCAGTCTAAGGAA 1946
DDB 37075 CTCAGCAATTTTGGTTAGATTAATGTTACGAAGGCTTTCTCGGATCTCCAGTCTAAGGAA 37134
QY 1947 ATGATAATGCCCTCCCTCTCAGCAATTTGGTATGATCCTTCTCCCTAAATTTAGAAAAGAAT 2006
DDB 37135 ATGATAATGCCCTCCCTCTCAGCAATTTGGTATGATCCTTCTCCCTAAATTTAGAAAAGAAT 37194
QY 2007 TTGGCATCTTAGAGAAATTAATGATCAAGGTATGATACCAAGATCAAGTAGTAAAT 2066
DDB 37195 TTGGCATCTTAGAGAAATTAATGATCAAGGTATGATACCAAGATCAAGTAGTAAAT 37254
QY 2067 GGGAAATTCAGGATTAATTCCTAGAGAAAGAGATATCCCAATATGTTTTTACAGAAATC 2126
DDB 37255 GGGAAATTCAGGATTAATTCCTAGAGAAAGAGATATCCCAATATGTTTTTACAGAAATC 37314
QY 2127 AATTCCTTACTTTAGACATCTTGAACCTTAACGCTGCTTTTGTAGCCTTCTCTAGCTGT 2185
DDB 37315 AATTCCTTACTTTAGACATCTTGAACCTTAACGCTGCTTTTGTAGCCTTCTCTAGCTGT 37374
QY 2186 TTTTCTCTGACAATTAATCTGTGTGTTTTTGTACATTTTGTAAATGTTTAAATAATTAAT 2245
DDB 37375 TTTTCTCTGACAATTAATCTGTGTGTTTTTGTACATTTTGTAAATGTTTAAATAATTAAT 37434
QY 2246 CTATATATATGTTTACATTAATGAATATATTGATTAATCTCTTTTGTAGATCCTGTTC 2305
DDB 37435 CTATATATATGTTTACATTAATGAATATATT - ATTACTTCTTTTGTAGATCCTGTTC 37493
QY 2306 CATTTGTGATCCTTATAGGAATAATCCTGTATGTTTTTGTGATGAGACGACATTTGGT 2365
DDB 37494 CATTTGTGATCCTTATAGGAATAATCCTGTATGTTTTTGTGATGAGACGACATTTGGT 37553
QY 2366 TTGTAATATCTAATCTGTGTCTTTCTTCATCCTTAAAAAATAAAACCATAGCCGGCGCGG 2425
DDB 37554 TTGTAATATCTAATCTGTGTCTTTCTTCATCCTTAAAAAATAAAACCATAGCCGGCGCGG 37613
QY 2426 TGGCTACGCGCTGTATCCAGACATTTTGGAGGCGGAGCGGGTGGATCATGAGTCTAG 2485
DDB 37614 TGGCTACGCGCTGTATCCAGACATTTTGGAGGCGGAGCGGGTGGATCATGAGTCTAG 37673
QY 2486 GAGATCGAGACCATCTCTGGCTAACAGGTGAAACCCCGTCTCTACTTAAAAATACAAAAA 2545
DDB 37674 GAGATCGAGACCATCTCTGGCTAACAGGTGAAACCCCGTCTCTACTTAAAAATACAAAAA 37733
QY 2546 TTAGCCGGGCGGCTGGCGGCGCTGTAGTCCAGCTTCTCGGAGGCTGAGGAGGAG 2605
DDB 37734 TTAGCCGGGCGGCTGGCGGCGCTGTAGTCCAGCTTCTCGGAGGCTGAGGAGGAG 37793
QY 2606 AATGGGCTGAACCCGGAGGCGGAGCTTGCAGTGAGCCCAAGATTGCGCCACTGCACTCCG 2665
DDB 37794 AATGGGCTGAACCCGGAGGCGGAGCTTGCAGTGAGCCCAAGATTGCGCCACTGCACTCCG 37853
QY 2666 CAGTCGGGCTGGCGGACAGGAGACTCTGTTCAAAAAATAAAAAAATAAAAAA 2725
DDB 37854 CAGTCGGGCTGGCGGACAGGAGACTCTGTCTC - AAAAAAATAAAAAAATAAAAAA 37912
QY 2726 ACCATAATAGGAAACGATCTTTACACTTAGGGTTTTGAGTTTTCTGTATCTATATAAAAA 2785
DDB 37913 ACCTTAAATGAGGAA - CATCTTTACACTTAGGGTTTTGAGTTTTCTGTATCTATATAAAAA 37970
QY 2786 GGGTTTGGATTAAGTGATCCCTGGCAGCTTATAAAAAATGTTAGGGCTTAATATTATTTCATAG 2845

DDB 37971 GGGTTTGGATTAAGTGATCCCTGGCAGCTTATAAAAAATGTTAGGGCTTAATATTATTTCATAG 38030
QY 2846 ATCGAGGATAGTTTCATTTCTTAGTCGCCCTTCTAGTCTACTCTTCTATACCAATCTGAGA 2905
DDB 38031 ATCGAGGATAGTTTCATTTCTTAGTCGCCCTTCTAGTCTACTCTTCTATACCAATCTGAGA 38090
QY 2906 CCATTTTACAATTTAGAAAAGACAAATAACTGGTTGGGTTACTTGCATAGTATAAACA 2965
DDB 38091 CCATTTTACAATTTAGAAAAGACAAATAACTGGTTGGGTTACTTGCATAGTATAAACA 38150
QY 2966 AGAAAAATAATTTTAGAGGGAATTAAGTTTGAACCAACATGTTTAAACAATTTCTACCAAG 3025
DDB 38151 AGAAAAATAATTTTAGAGGGAATTAAGTTTGAACCAACATGTTTAAACAATTTCTACCAAG 38210
QY 3026 TGGGATTTGCCCTGTGATTTAAAGATGCTGTAAACATTTTGGGCCAGTAGTTATAAATTTGAAA 3085
DDB 38211 TGGGATTTGCCCTGTGATTTAAAGATGCTGTAAACATTTTGGGCCAGTAGTTATAAATTTGAAA 38270
QY 3086 AATGTTTATAGCCAATATATAATTTTATTTAAATATACAGTTTTCATCAGTCTATTAGT 3145
DDB 38271 AATGTTTATAGCCAATATATAATTTTATTTAAATATACAGTTTTCATCAGTCTATTAGT 38330
QY 3146 ATTTTCATTTAAGTCTAAGATGCCATCAGTGGTTAGCAAAACACACTGTTTTATGCACTGCT 3205
DDB 38331 ATTTTTCATTTAAGTCTAAGATGCCATCAGTGGTTAGCAAAACACACTGTTTTATGCACTGCT 38390
QY 3206 AAGAAAGAAATAAGGGCTGTGTGCACTGCTCACACCTGTGGGAGCCCAAGGAGGAGCA 3265
DDB 38391 AAGAAAGAAATAAGGGCTGTGTGCACTGCTCACACCTGTGGGAGCCCAAGGAGGAGCA 38450
QY 3266 TCACCTTGAGGCCAGAAAGTTCAAGACCAACCTGGTCAACATTTGTAGACCCCTGTCTCTACA 3325
DDB 38451 TCACCTTGAGGCCAGAAAGTTCAAGACCAACCTGGTCAACATTTGTAGACCCCTGTCTCTACA 38510
QY 3326 AAAAAAATAAGTTAAAAAATTAGCTGGGTGGCGGCACATGCTGTAGTTCCTGAGCTACT 3385
DDB 38511 AAAAAAATAAGTTAAAAAATTAGCTGGGTGGCGGCACATGCTGTAGTTCCTGAGCTACT 38570
QY 3386 CTGGAGGCTAGGTTGGGAGGATTTGCTAGAGCCACCGTGTGGAAGCTGCAATAGAGCTGTG 3445
DDB 38571 CTGGAGGCTAGGTTGGGAGGATTTGCTAGAGCCACCGTGTGGAAGCTGCAATAGAGCTGTG 38630
QY 3446 ACCACACCACTGCGCTCCAGCGTGGGCAACAGAGTGAGACCTGTTTCTTAAAGAAAGAA 3505
DDB 38631 ACCACACCACTGCGCTCCAGCGTGGGCAACAGAGTGAGACCTGTTTCTTAAAGAAAGAA 38690
QY 3506 AGAAAAAGGGCTGCCACTTAAACAGACACACTATTGAGTTGAGTACCCCTGATTTCAAA 3565
DDB 38691 AG - AAAAAAGGGCTGCCACTTAAACAGACACACTATTGAGTTGAGTACCCCTGATTTCAAA 38749
QY 3566 GACATGAAAATGTTAAATATAGCCACCTTGAAGCTTTTCAGGSCCCTTTCTACCCCTGAAT 3625
DDB 38750 GACATGAAAATGTTAAATATAGCCACCTTGAAGCTTTTCAGGSCCCTTTCTACCCCTG - ATT 38807
QY 3626 AACAGTGACATTTGGACCACTCTCTCTTACTTCTTATCTTCTTAAATATACCCCAAAACAG 3685
DDB 38808 AACAGTGACATTTGGACCACTCTCTCTTACTTCTTATCTTCTTAAATATACCCCAAAACAG 38867
QY 3686 AATGAGTTGATTCATAGGCAATGAAGGATCTCATTTCTTCCCTTCACCATCAGTATTGTTGGT 3745
DDB 38868 AATGAGTTGATTCATAGGCAATGAAGGATCTCATTTCTTCCCTTCACCATCAGTATTGTTGGT 38927
QY 3746 TAAAAATTTTATTTATAGTTTTTCAGACAAATCGTTTGTGCTTAATCTTATCT - - - -TTGCAATT 3801
DDB 38928 TAAAAATTTTATTTATAGTTTTTCAGACAAATCGTTGCTTAATCTTATCTGGAAGTGCAATT 38987
QY 3802 TTGTATGTTTCTCTGCTATTCTCTTATCTCTTACTTCTTATCTTAAATATACCCCAAAACAG 3861
DDB 38988 TTGTATGTTTCTCTGCTATTCTCTTATCTCTTATAGCACTCAGGCAAGTAGGAGTGGCTGAAA 39047
QY 3862 GTTTGTTGAGTTTTTGGAGTGGAGTTTCAAAATTTATCTATAGTTGATCGAAGTCAAT 3921

Db 39048 GTTGTGAGTTTGTGGAAGTGGAGTTTACAAATATCTATAGTTGATGCAACTACAAT 39107
QY 3922 ACCAAACATGTGTCGGGAATATGTGTGCTATCCTCAGCTTTTTCCTGTGACATGTGAC 3981
Db 39108 AGCAACATGTGTCGGGAATATGTGTGCTATCCTCAGCTTTTTCCTGTGACATGTGAC 39167
QY 3982 ATTAACACATTTAGAACATACAGGTGAAGAATAAAGATCACTAGATAAACAATGTATAC 4041
Db 39168 ATTAACACATTTAGAACATACAGGTGAAGAATAAAGATCACTAGATAAACAATGTATAC 39227
QY 4042 ATTTCCAAATGTGTTGATAATATTTTAAATATCTACCTTATCCATGTATTTTACTACT 4101
Db 39228 ATTTCCAAATGTGTTGATAATATTTTAAATATCTACCTTATCCATGTATTTTACTACT 39287
QY 4102 CACAAAATACATATGTGTGAACACAACTTTCAAGCAACATCAGATGCTTTTAAGA 4161
Db 39288 CACAAAATACATATGTGTGAACACAACTTTCAAGCAACATCAGATGCTTTTAAGA 39347
QY 4162 GTGTTGTGTCCTCAACCTAGTTCCCTGTGACACATTTGAAGCAATTTAAAGGAATAT 4221
Db 39348 GTGTTGTGTCCTGAACCTAGTTCCCTGTGACACATTTGAAGCAATTTAAAGGAATAT 39407
QY 4222 TCAAAACCATTTGATCTGACTGACTGTTT-CCATAATGATGGATACCTCCCTCTACT 4280
Db 39408 TCAAAACCATTTGATCTGACTGACTGTTTCCCTATAATGATGGATACCTCCCTCTACT 39467
QY 4281 TAGGGGTGATAGG-TGCAATTTAAGGATCAGCCCTTAAACATATTCACAGCAGTCCCC 4339
Db 39468 TAGGGGTGATAGGTTGCAATTTAATGGAAGTACGCTTTAAACATATTCACAGCAGTCCCC 39527
QY 4340 TTCT 4343
Db 39528 TTCT 39531

RESULT 3
US-60-243-742-99
; Sequence 99, Application us/60243742
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000933
; CURRENT APPLICATION NUMBER: US/60/243,742
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 378
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 62724
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(62724)
; OTHER INFORMATION: n = A,T,C or G
US-60-243-742-99

Query Match 74.8%; Score 3248.4; DB 68; Length 62724;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 3427; Conservative 3; Mismatches 34; Indels 20; Gaps 14;
QY 872 TTCCTGGGTGGGGGTGGAGGCAATTTGAACAGAGCAGTTATGCTTGGTCTGCCAGTTT 931
Db 36056 TTATTACGTTAGGGGTGGAGGCAATTTGAACAGAGCAGTTATGCTTGGTCTGCCAGTTT 36115
QY 932 CTCCTTACTTACAGAGGTGGTGGATGAGTTAACTGGGTTCATCAACCCCTTTTGTTA 991
Db 36116 CTCCTTACTTACAGAGGTGGTGGATGAGTTAACTGGGTTCATCAACCCCTTTTGTTA 36175
QY 992 CAT-CCATAGATGTTCTCTGTTATACAAAGGTAAGTTAAGTTGGTGGTCTATG 1050
Db 36176 CATCCCATAGATGTTCTCTGTTATACAAAGGTAAGTTAAGTTGGTGGTCTATG 36235

QY 1051 ACTTACTGAACATTTATTTTATAAAAAATGAAGAGCTCTATGAGAGCAGGGATTTGGGTT 1110
Db 36236 ACTTACTGAACATTTATTTTATAAAAAATGAAGAGCTCTATGAGAGCAGGGATTTGGGTT 36295
QY 1111 CATTACTGCATCCTCAGGTCCTCTGACGTTAGCCACATCATATGTTATCATAGTAATA 1170
Db 36296 CATTACTGCATCCTCAGGTCCTCTGACGTTAGCCACATCATATGTTATCATAGTAATA 36355
QY 1171 ACAACAAACAGACATTTAGTTTGTACTATAAATAACAAGAAATTTGTTGTTTCACTT 1230
Db 36356 ACAACAAACAGACATTTAGTTTGTACTATAAATAACAAGAAATTTGTTGTTTCACTT 36415
QY 1231 ATGTTAGCTCATTTAGTTCCTTATAACAAGCCTGTGAGATGGATCTATTACTTCTCAT 1290
Db 36416 ATGTTAGCTCATTTAGTTCCTTATAACAAGCCTGTGAGATGGATCTATTACTTCTCAT 36475
QY 1291 TGTAACTCTGAGAAAACTAAGGTACAGTAGGGTTTGTAGTCTACCAAGGGTCGAAAGC 1350
Db 36476 TGTAACTCTGAGAAAACTAAGGTACAGTAGGGTTTGTAGTCTACCAAGGGTCGAAAGC 36535
QY 1351 CTGAGTA-TAAGGGTAGACAAAGATTCAGGCACTGAGATTTCTTTGAGTCTATGT---CT 1406
Db 36536 CTGAGTAGTAAGGGGTAGACAAAGATTCAGGCACTGAGATTTCTTTGAGTCTATGTCTT 36595
QY 1407 AACCATTTATGCCCTTATAGTGCCTTGTTCCTTAAATAAACACTGTGCTGACTACATATTT 1466
Db 36596 AACCATTTATGCCCTTATAGTGCCTTGTTCCTTAAATAAACACTGTGCTGACTACATATTT 36655
QY 1467 TTTTCTCTTTTAACTTGAATTTAAAAAAGATTTAGCAAAAGTTGATGTCGTC 1526
Db 36656 TTTTCTCTTTTAACTTGAATTTAAAAAAGATTTAGCAAAAGTTGATGTCGTC 36714
QY 1527 TTTTAAATTAATTTATGCGCGTTAGAAACTGTTGCTCTACTAAGTAAATGCTTTCAAAAAC 1586
Db 36715 TTTTAAATTAATTTATGCGCGTTAGAAACTGTTGCTCTACTAAGTAAATGCTTTCAAAAAC 36774
QY 1587 ATGAGCTGTAGAAATGTGATATATCATTTTCTGTCGCGCTTTTAAACATTTCTCTGATTT 1646
Db 36775 ATGAGCTGTAGAAATGTGATATATCATTTTCTGTCGCGCTTTTAAACATTTCTCTGATTT 36834
QY 1647 ATATGTTAAAAATCTCTCTCTGAAATTTTAAATACTGCTTCAAGATTTCAATACATA 1706
Db 36835 ATATGTTAAAAATCTCTCTCTGAAATTTTAAATACTGCTTCAAGATTTCAATACATA 36894
QY 1707 CACTGAGCTTTGTTAAGCATATTAATACACAGGCTCAGGATTTCTTAGTGAACAATAAT 1766
Db 36895 CACTGAGCTTTGTTAAGCATATTAATACACAGGCTCAGGATTTCTTAGTGAACAATAAT 36954
QY 1767 TGTAACTCTTCTCCTAAATGTCTGGCCTTTGCTAACTTTATTTTAAATGATTAATCCTA 1826
Db 36955 TGTAACTCTTCTCCTAAATGTCTGGCCTTTGCTAACTTTATTTTAAATGATTAATCCTA 37014
QY 1827 TTTTGTAAATGATGTACCTGGAATAATGTTCCACATATATTTCCAAATTTGAGTCCCAAT 1886
Db 37015 TTTTGTAAATGATGTACCTGGAATAATGTTCCACATATATTTCCAAATTTGAGTCCCAAT 37074
QY 1887 CTCAGCATTTTGGTTAGATTTATGTTACGAAGGCTTTCTGATCTCCAGTCTAAGGAA 1946
Db 37075 CTCAGCATTTTGGTTAGATTTATGTTACGAAGGCTTTCTGATCTCCAGTCTAAGGAA 37134
QY 1947 ATGATATGCTCCTCTCAGCATTTGGTATGATCTTCTTCCCTAATTTAGAAAAGAT 2006
Db 37135 ATGATATGCTCCTCTCAGCATTTGGTATGATCTTCTTCCCTAATTTAGAAAAGAT 37194
QY 2007 TTGSCATCTTAGAGAAATTTATGATTCACGATATGATACCAAAAGATCAAGTAGTAATTT 2066
Db 37195 TTGSCATCTTAGAGAAATTTATGATTCACGATATGATACCAAAAGATCAAGTAGTAATTT 37254
QY 2067 GGGAAATTCAGGATTTATTCCTAGAGAAAAGGATATCCCATATATGTTTTTACAGAAATC 2126
Db 37255 GGGAAATTCAGGATTTATTCCTAGAGAAAAGGATATCCCATATATGTTTTTACAGAAATC 37314

Db 39468 TAGGGTCATAGTGGTCAATTTAATGAAGTCAGCCTTAAACATATTACAGCAGTCCCC 39527

QY 4340 TTCT 4343
Db 39528 TTCT 39531

RESULT 4
US-09-654-935A-257
; Sequence 257, Application US/09654935A
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Zhiwei
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 793
; CURRENT APPLICATION NUMBER: US/09/654,935A
; CURRENT FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: pt_FL-genes Version 1.0
; SEQ ID NO 257
; LENGTH: 3280
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2892)

US-09-654-935A-257

Query Match 23.6%; Score 1023; DB 25; Length 3280;
Best Local Similarity 100.0%; Pred. No. 9.5e-111;
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGCCGCCAAAAGCAGGATACGCTTTGAGTACCTATTGAAACATTAATGACAGT 60
Db 1 ATGGAGCCGCCAAAAGCAGGATACGCTTTGAGTACCTATTGAAACATTAATGACAGT 60
QY 61 TCACATAAGAAGTTCTTCATGATATCTAACTTGGCACCAGATGATGTTCTGCCTTAC 120
Db 61 TCACATAAGAAGTTCTTCATGATATCTAACTTGGCACCAGATGATGTTCTGCCTTAC 120
QY 121 TCAATACGGGTCTTGTGGAAGCTGCTGTACCAAAATGTTGATGGCTTTTAAATGAAGA 180
Db 121 TCAATACGGGTCTTGTGGAAGCTGCTGTACCAAAATGTTGATGGCTTTTAAATGAAGA 180
QY 181 GAAGATGTTATGAACATTTAGACTGGAAACCAACAAAGCAATGTTGAAGTGCCTTT 240
Db 181 GAAGATGTTATGAACATTTAGACTGGAAACCAACAAAGCAATGTTGAAGTGCCTTT 240
QY 241 TTCCCTGCCCGTGTCTTCTCAAGATTTTACTGGAATACCAAGCAATGTTGATTTTGT 300
Db 241 TTCCCTGCCCGTGTCTTCTCAAGATTTTACTGGAATACCAAGCAATGTTGATTTTGT 300
QY 301 GCTATGAGGAGGAGTGAAGTCTTGGAGGTGATCTGGAAGTCCATCCCTCTTGT 360
Db 301 GCTATGAGGAGGAGTGAAGTCTTGGAGGTGATCTGGAAGTCCATCCCTCTTGT 360
QY 361 CCGACAGATCTTACAGTTGACCATTTCTTACAAATTTGACTTCAGTAAATGTGCAATACAG 420
Db 361 CCGACAGATCTTACAGTTGACCATTTCTTACAAATTTGACTTCAGTAAATGTGCAATACAG 420
QY 421 ATGACACAAATCTCGGAGGTGGTGACCTGCAGAAAGCAAGCAAGTCTCTCCACCTTAA 480
Db 421 ATGACACAAATCTCGGAGGTGGTGACCTGCAGAAAGCAAGCAAGTCTCTCCACCTTAA 480

Db 421 AATGCACAAATCCTGGAGTGGTGACCTGCAGAAAGCAAGCAAGTCTCTCCACCTTAA 480
QY 481 GTGCAGCTTAAGAGCTTCCCTGCAGAGGCCAGACTACCTGCGAGGATCTTCTGATTTCT 540
Db 481 GTGCAGCTTAAGAGCTTCCCTGCAGAGGCCAGACTACCTGCGAGGATCTTCTGATTTCT 540
QY 541 GGAGAACTAGCCGAAACTCAGGAACATTTTCTTCAGATTCAGAAATACACCCATCTCG 600
Db 541 GGAGAACTAGCCGAAACTCAGGAACATTTTCTTCAGATTCAGAAATACACCCATCTCG 600
QY 601 TGTCTTTTTCATTTGCAACAGTGCCTGAAACCTGAAACAGTGTAAATAACAAGTA 660
Db 601 TGTCTTTTTCATTTGCAACAGTGCCTGAAACCTGAAACAGTGTAAATAACAAGTA 660
QY 661 GAATTCGCGAGAAATCGAGAGAGGCTTTCAGTCTTTTAAAGTGGAGTTCAGAGTCTTAAAG 720
Db 661 GAATTCGCGAGAAATCGAGAGAGGCTTTCAGTCTTTTAAAGTGGAGTTCAGAGTCTTAAAG 720
QY 721 AATGTGCGAGTATCCCTCTCGAACTGGAATGCAATGCTCATCAATAAATAGATTTTG 780
Db 721 AATGTGCGAGTATCCCTCTCGAACTGGAATGCAATGCTCATCAATAAATAGATTTTG 780
QY 781 TCAAGAGTGGTTTTGAAAGAAAGACCTCTCTCCACAGACAGTGTAGTCGACAGAT 840
Db 781 TCAAGAGTGGTTTTGAAAGAAAGACCTCTCTCCACAGACAGTGTAGTCGACAGAT 840
QY 841 TCACACATAACGATGTTGATGTTTGGGTTAGGATCTGCGGTTGGAGGATTTGAA 900
Db 841 TCACACATAACGATGTTGATGTTTGGGTTAGGATCTGCGGTTGGAGGATTTGAA 900
QY 901 ACAGAAGCAGTTATGCTTGGTCTGCCAGTTTCTTACTTTACCAGAGTGTGGATGT 960
Db 901 ACAGAAGCAGTTATGCTTGGTCTGCCAGTTTCTTACTTTACCAGAGTGTGGATGT 960
QY 961 GAGTTAACTGGTCATCAAAACCTTTTGTACATCCATAGATGTTCTTGTGATATACA 1020
Db 961 GAGTTAACTGGTCATCAAAACCTTTTGTACATCCATAGATGTTCTTGTGATATACA 1020
QY 1021 AAG 1023
Db 1021 AAG 1023

RESULT 5

PCT-US01-08656-4031
; Sequence 4031, Application PC/TUS0108656
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: PCT/US01/08656
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 4031
; LENGTH: 3290
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1)..(1869)
; OTHER INFORMATION: 97% homologous to Homo sapiens iron-responsive element-
; OTHER INFORMATION: binding protein/iron regulatory protein 2, accession number
; OTHER INFORMATION: M58511.Smith-Waterman Score=3141.
PCT-US01-08656-4031

Query Match 23.6%; Score 1023; DB 1; Length 3290;
Best Local Similarity 100.0%; Pred. No. 9.5e-111;
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGACGCCCAAGCAGGATAGCCCTTTGAGTACCTTTATTTGAACATTAATGACAGT 60
Db 1 ATGACGCCCAAGCAGGATAGCCCTTTGAGTACCTTTATTTGAACATTAATGACAGT 60
QY 61 TCACATAAGAAGTCTTCGATGTATCTAACTTGGCCACCAGATGATGTTCTGCCCTTAC 120
Db 61 TCACATAAGAAGTCTTCGATGTATCTAACTTGGCCACCAGATGATGTTCTGCCCTTAC 120
QY 121 TCATACCGGCTGTGTTGGAGGCTGTCTAGGAAATGTGATGCTTTTAAATCAAGAAG 180
Db 121 TCATACCGGCTGTGTTGGAGGCTGTCTAGGAAATGTGATGCTTTTAAATCAAGAAG 180
QY 181 GAAGATGTTATGAACATTTTAGACTGGAACCAACCAAGCAATGTTGAAGTCCCTTT 240
Db 181 GAAGATGTTATGAACATTTTAGACTGGAACCAACCAAGCAATGTTGAAGTCCCTTT 240
QY 241 TTCCCTGCCCGTGTCTTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTGCT 300
Db 241 TTCCCTGCCCGTGTCTTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTGCT 300
QY 301 GCTATGAGGAGGAGTCAAAACHTCTTGGAGGTGATCCTGAGAAAGTCCATCCTGCTGT 360
Db 301 GCTATGAGGAGGAGTCAAAACHTCTTGGAGGTGATCCTGAGAAAGTCCATCCTGCTGT 360
QY 361 CCGACAGATCTTACAGTTGACCATTTTACAAATTTGACTTCAGTAAATGTGCAATACAG 420
Db 361 CCGACAGATCTTACAGTTGACCATTTTACAAATTTGACTTCAGTAAATGTGCAATACAG 420
QY 421 AATGACCAAACTCTGGAGGTGGTGACCTGCAGAAAGCAGGAAAGCTCTCCACTTAAA 480
Db 421 AATGACCAAACTCTGGAGGTGGTGACCTGCAGAAAGCAGGAAAGCTCTCCACTTAAA 480
QY 481 GTGACGCTAAGAGCTTCCCTGCAGAGGCCAGACTACCTGCCAGGATCTTGTGATTTCT 540
Db 481 GTGACGCTAAGAGCTTCCCTGCAGAGGCCAGACTACCTGCCAGGATCTTGTGATTTCT 540
QY 541 GGAGAACTAGCGCCGAAACTCAGGAACATTTTCTTCGAGATTTGAGATACACCCATCCTG 600
Db 541 GGAGAACTAGCGCCGAAACTCAGGAACATTTTCTTCGAGATTTGAGATACACCCATCCTG 600
QY 601 TGTCCTTTTCAATTTGCAACACAGTGCCTGAACTGAAACAGTGTAAAAATCAAGAAGTA 660
Db 601 TGTCCTTTTCAATTTGCAACACAGTGCCTGAACTGAAACAGTGTAAAAATCAAGAAGTA 660
QY 661 GAAATCGGCAGAAATCGAGAGAGGCTTCAGTTTTTAAAGTGGAGTTTCAAGAGTTTAAAG 720
Db 661 GAAATCGGCAGAAATCGAGAGAGGCTTCAGTTTTTAAAGTGGAGTTTCAAGAGTTTAAAG 720
QY 721 AATGTGGCAGTATCCCTCCCTGGAACTGGAATGGCTCATCAATAAACTTAGAATATTGG 780
Db 721 AATGTGGCAGTATCCCTCCCTGGAACTGGAATGGCTCATCAATAAACTTAGAATATTGG 780
QY 781 TCAAGAGTGGTTTTTGAAGAAAAAGACCTCCTCTTCCAGACAGTGTAGTGGGACAGAT 840
Db 781 TCAAGAGTGGTTTTTGAAGAAAAAGACCTCCTCTTCCAGACAGTGTAGTGGGACAGAT 840
QY 841 TCACACATAACGATGGTGAATGGTTTTAGGGATTTCTGGGTTGGGGGTTGGAGGCAATTGAA 900
Db 841 TCACACATAACGATGGTGAATGGTTTTAGGGATTTCTGGGTTGGGGGTTGGAGGCAATTGAA 900
QY 901 ACAGAGCAGTATGCTTGGTCTGCCAGTTTCTTACTTTTACCAGAGGTGGTTGGATGT 960
Db 901 ACAGAGCAGTATGCTTGGTCTGCCAGTTTCTTACTTTTACCAGAGGTGGTTGGATGT 960
QY 961 GAGTTAACTGGGTCATCAAAACCCCTTTTGTATACATCCATAGATGTTGTTCTTGGTATTACA 1020
Db 961 GAGTTAACTGGGTCATCAAAACCCCTTTTGTATACATCCATAGATGTTGTTCTTGGTATTACA 1020
QY 1021 AAG 1023
Db 1021 AAG 1023
```

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RESULT 6
US-09-359-922-8303
; Sequence 8303, Application US/09359922
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; LIBRARIES
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/359,922
; CURRENT FILING DATE: 1999-07-22
; EARLIER APPLICATION NUMBER: US 09/205,155
; EARLIER FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 13203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8303
; LENGTH: 4684
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)....(4684)
; OTHER INFORMATION: n = A,T,C or G
US-09-359-922-8303

Query Match      23.6%; Score 1023; DB 17; Length 4684;
Best Local Similarity 100.0%; Pred. No. 9,1e-111;
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACGCCCAAGCAGGATAGCCCTTTGAGTACCTTTATTTGAACATTAATGACAGT 60
Db 13 ATGACGCCCAAGCAGGATAGCCCTTTGAGTACCTTTATTTGAACATTAATGACAGT 72
QY 61 TCACATAAGAAGTCTTCGATGTATCTAACTTGGCCACCAGATGATGTTCTGCCCTTAC 120
Db 73 TCACATAAGAAGTCTTCGATGTATCTAACTTGGCCACCAGATGATGTTCTGCCCTTAC 132
QY 121 TCAATACGGGCTGTGTTGGAGGCTGTCTGACGAAATTTGTGATGGCTTTTAAATGAAGAAG 180
Db 133 TCAATACGGGCTGTGTTGGAGGCTGTCTGACGAAATTTGTGATGGCTTTTAAATGAAGAAG 192
QY 181 GAAGATGTTATGAACATTTTATAGACTGGAACCAACCAAGCAATGTTGAAGTGCCTTT 240
Db 193 GAAGATGTTATGAACATTTTATAGACTGGAACCAACCAAGCAATGTTGAAGTGCCTTT 252
QY 241 TTCCCTGCCCGTGTCTTCTTCAAGATTTTACTGGAATACCAGCAATGTTGATTTGCT 300
Db 253 TTCCCTGCCCGTGTCTTCTTCAAGATTTTACTGGAATACCAGCAATGTTGATTTGCT 312
QY 301 GCTATGAGGAGGAGGCTGAAACTCTTGGAGGTGATCCTGAGAAAGTCCATCCTGCTTCT 360
Db 313 GCTATGAGGAGGAGGCTGAAACTCTTGGAGGTGATCCTGAGAAAGTCCATCCTGCTTCT 372
QY 361 CCGACAGATCTTACAGTTGACCATTTCTTACAAATTTGACTTCAGTAAATGTGCAATACAG 420
Db 373 CCGACAGATCTTACAGTTGACCATTTCTTACAAATTTGACTTCAGTAAATGTGCAATACAG 432
QY 421 AATGCACCAATCCTCGAGGTGGTGACCTGCGAGAGGAGGAAAGCTCTCCACTTAAA 480
Db 433 AATGCACCAATCCTCGAGGTGGTGACCTGCGAGAGGAGGAAAGCTCTCTCCACTTAAA 492
QY 481 GTGCAGCCTAAGAAGCTTCCCTGCAGAGGCCAGACTACCTGCCGAGAGTCTTGTGATTTCT 540
Db 493 GTGCAGCCTAAGAAGCTTCCCTGCAGAGGCCAGACTACCTGCCGAGAGTCTTGTGATTTCT 552
QY 541 GGAGAACTAGGCCGAAACTCAGGAACATTTTCTTCGAGATTTGAGAAATACACCCATCCTG 600
Db 553 GGAGAACTAGGCCGAAACTCAGGAACATTTTCTTCGAGATTTGAGAAATACACCCATCCTG 612
QY 601 TGTCCTTTTCAATTTGCAACACAGTGCCTGACCTGGAACAGTGTAAAAATCAAGAAGTA 660
Db 613 TGTCCTTTTCAATTTGCAACACAGTGCCTGACCTGGAACAGTGTAAAAATCAAGAAGTA 672
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QY 661 GAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTTTAAAGTGAAGTTTAAAG 720
|||||
Db 673 GAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTTTAAAGTGAAGTTTAAAG 732
QY 721 AATGTGGCAGTATCCCTCGGAACTGGAATGCTCATCAATAAATAGATTTAG 780
|||||
Db 733 AATGTGGCAGTATCCCTCGGAACTGGAATGCTCATCAATAAATAGATTTAG 792
QY 781 TCAAGAGTGGTTTTTGAAGAAAGACCTCTCTTCCAGACAGTGTAGTCGGCACAGAT 840
|||||
Db 793 TCAAGAGTGGTTTTTGAAGAAAGACCTCTCTTCCAGACAGTGTAGTCGGCACAGAT 852
QY 841 TCACACATAACGATGGTGAATGGTTAGGATCTCTGGGGTGGGGTGGAGGCAATGAA 900
|||||
Db 853 TCACACATAACGATGGTGAATGGTTAGGATCTCTGGGGTGGGGTGGAGGCAATGAA 912
QY 901 ACAGAAGCAGTATGCTTGGTCTGCCAGTTCTCTTACTTTACCAGAGGTGGTTGGATGT 960
|||||
Db 913 ACAGAAGCAGTATGCTTGGTCTGCCAGTTCTCTTACTTTACCAGAGGTGGTTGGATGT 972
QY 961 GAGTTAACTGGGTCTATCAAAACCTTTTGTATCATCCATAGATGTTGTTGGTATTACA 1020
|||||
Db 973 GAGTTAACTGGGTCTATCAAAACCTTTTGTATCATCCATAGATGTTGTTGGTATTACA 1032
QY 1021 AAG 1023
|||
Db 1033 AAG 1035

RESULT 7

US-09-359-922-8303
; Sequence 8303, Application US/0935922A
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Liu, Jin
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; FILE OF INVENTION: LIBRARIES
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/359,922A
; EARLIER FILING DATE: 1999-07-22
; EARLIER FILING DATE: 1998-12-03
; EARLIER FILING DATE: 1998-12-03
; EARLIER FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 13203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8303
; LENGTH: 4684
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4684)
; OTHER INFORMATION: n = A,T,C or G
US-09-359-922-8303

Query Match 23.6%; Score 1023; DB 17; Length 4684;
Best Local Similarity 100.0%; Pred. No. 9, 1e-111;
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACGCCCAAGCAGGATACGCCCTTTGAGTACCTTATTGAAACATTAATGACAGT 60
Db 13 ATGGACGCCCAAGCAGGATACGCCCTTTGAGTACCTTATTGAAACATTAATGACAGT 72
QY 61 TCACATAGAGTTCCTCGATGTATCTAAACTTGGCACCAGATGATGTCGCTTAC 120
Db 73 TCACATAGAGTTCCTCGATGTATCTAAACTTGGCACCAGATGATGTCGCTTAC 132
QY 121 TCAATACGGGTCTGTTGGAACTGCTGTACGAAATTTGATGGCTTTTAAATGAAGAAG 180
Db 133 TCAATACGGGTCTGTTGGAACTGCTGTACGAAATTTGATGGCTTTTAAATGAAGAAG 192
QY 181 GAAGATGTTATGAACATTTTATAGACTGGAAACCAACAAAGCAATGTTGAAGTGCCCTTT 240

Db 193 GAAGATGTTATGAACATTTTAGACTGGAAACCAACAAAGCAATGTTGAAGTGCCCTTT 252
QY 241 TTCCCTGCCCGTCTTCTTCAAGATTTTACTGGAAATACCAGCAATGGTGAATTTGCT 300
Db 253 TTCCCTGCCCGTCTTCTTCAAGATTTTACTGGAAATACCAGCAATGGTGAATTTGCT 312
QY 301 GCTATGAGGAGGACAGTGAACACTCTTGGAGGTGATCTCTGAGAAAGTCCATCTGCTTGT 360
Db 313 GCTATGAGGAGGACAGTGAACACTCTTGGAGGTGATCTCTGAGAAAGTCCATCTGCTTGT 372
QY 361 CCACAGATCTTACAGTTGACCAATCTTTACAAATTTGACTTCAGTAAATGTCGAATACAG 420
Db 373 CCACAGATCTTACAGTTGACCAATCTTTACAAATTTGACTTCAGTAAATGTCGAATACAG 432
QY 421 AATGCAACCAATCTCGAGGTGGTGAACCTGCAGAAAGCAGGAAGCTCTCTCCACTTAA 480
Db 433 AATGCAACCAATCTCGAGGTGGTGAACCTGCAGAAAGCAGGAAGCTCTCTCCACTTAA 492
QY 481 GTGACGCTAAGAGCTTCCCTGCGAGGCGCAGACTACCTGCGGAGGATCTTTGTGATCT 540
Db 493 GTGACGCTAAGAGCTTCCCTGCGAGGCGCAGACTACCTGCGGAGGATCTTTGTGATCT 552
QY 541 GGAGAACTAGGCGGAAACTCAGGAACATTTCTTCGAGATTGAGAAATACACCCATCCTG 600
Db 553 GGAGAACTAGGCGGAAACTCAGGAACATTTCTTCGAGATTGAGAAATACACCCATCCTG 612
QY 601 TGTCTTTTCAATTTGCAACCACTGCTGAACCTGAAACAGTGTAAAAATCAAGAATGA 660
Db 613 TGTCTTTTCAATTTGCAACCACTGCTGAACCTGAAACAGTGTAAAAATCAAGAATGA 672
QY 661 GAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTTTAAAGTGAAGTTTAAAG 720
Db 673 GAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTTTAAAGTGAAGTTTAAAG 732
QY 721 AATGTGGCAGTATCCCTCTCGAATGGAATGGCTCATCAATAAATAGATTTAG 780
Db 733 AATGTGGCAGTATCCCTCTCGAATGGAATGGCTCATCAATAAATAGATTTAG 792
QY 781 TCAAGAGTGGTTTTTGAAGAAAGACCTCTCTTCCAGACAGTGTAGTCGGCACAGAT 840
Db 793 TCAAGAGTGGTTTTTGAAGAAAGACCTCTCTTCCAGACAGTGTAGTCGGCACAGAT 852
QY 841 TCACACATAACGATGGTGAATGGTTAGGATCTCTTACTTTACCAGAGGTGGTGGATGT 900
Db 853 TCACACATAACGATGGTGAATGGTTAGGATCTCTTACTTTACCAGAGGTGGTGGATGT 912
QY 901 ACAGAAGCAGTATGCTTGGTCTGCCAGTTCTCTTACTTTACCAGAGGTGGTGGATGT 960
Db 913 ACAGAAGCAGTATGCTTGGTCTGCCAGTTCTCTTACTTTACCAGAGGTGGTGGATGT 972
QY 961 GAGTTAACTGGGTCTATCAAAACCTTTTGTATCATCCATAGATGTTGTTGGTATTACA 1020
Db 973 GAGTTAACTGGGTCTATCAAAACCTTTTGTATCATCCATAGATGTTGTTGGTATTACA 1032
QY 1021 AAG 1023
|||
Db 1033 AAG 1035

RESULT 8

US-09-919-002-8303
; Sequence 8303, Application US/09919002
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Liu, Jin
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; FILE OF INVENTION: LIBRARIES
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/919,002
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922
; PRIOR FILING DATE: FILING DATE: 1999-07-22

;; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 09/034,341
;; PRIOR FILING DATE: FILING DATE: 1998-02-13
;; NUMBER OF SEQ ID NOS: 13203
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 8303
;; LENGTH: 4684
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(4684)
;; OTHER INFORMATION: n = A,T,C or G
US-09-919-002-8303

Query Match 23.6%; Score 1023; DB 34; Length 4684;
Best Local Similarity 100.0%; Pred. No. 9.1e-111; Indels 0; Gaps 0;
Matches 1023; Conservative 0; Mismatches 0;

QY 1 ATGGACGCCCAAGCAGGATAGCCCTTTGAGTACCTTTATTAACATTAATGACAGT 60
DB 13 ATGGACGCCCAAGCAGGATAGCCCTTTGAGTACCTTTATTAACATTAATGACAGT 72
QY 61 TCACATAGAAGTCTTCGATGATCTAAACTTGGCACCAGATGATGTTCTGCCCTTAC 120
DB 73 TCACATAGAAGTCTTCGATGATCTAAACTTGGCACCAGATGATGTTCTGCCCTTAC 132
QY 121 TCAATACGGGTCTTTGGAGGCTGTGTAGAAATTTGATGGCTTTTAAATCAAGAAG 180
DB 133 TCAATACGGGTCTTTGGAGGCTGTGTAGAAATTTGATGGCTTTTAAATCAAGAAG 192
QY 181 GAAGATGTTATGAACATTTTAGCTGGAAACCAACCAAGCAATGTTGAAGTGCCCTTT 240
DB 193 GAAGATGTTATGAACATTTTAGCTGGAAACCAACCAAGCAATGTTGAAGTGCCCTTT 252
QY 241 TTCCCTGCCGTGTTCTTCAAGATTTTACTGGAAATACAGCAATGTTGGATTTGCT 300
DB 253 TTCCCTGCCGTGTTCTTCAAGATTTTACTGGAAATACAGCAATGTTGGATTTGCT 312
QY 301 GCTATGAGGAGGAGGAGTGAACCTCTTGGAGGTGATCCTCAGAAAGTCCATCTGCTTGT 360
DB 313 GCTATGAGGAGGAGGAGTGAACCTCTTGGAGGTGATCCTCAGAAAGTCCATCTGCTTGT 372
QY 361 CCGACAGATCTTACAGTTGACCAATTTTACAAATTCAGTTCAGTAAATGCAATACAG 420
DB 373 CCGACAGATCTTACAGTTGACCAATTTTACAAATTCAGTTCAGTAAATGCAATACAG 432
QY 421 AATGCCACCAATCTGAGGTGTTGACCTCGAGAAACAGCAAGCTCTCCACCTTAA 480
DB 433 AATGCCACCAATCTGAGGTGTTGACCTCGAGAAACAGCAAGCTCTCCACCTTAA 492
QY 481 GTGAGGCTTAAGAAGCTTCCCTCGAGAGGCCAGCTACCTGCCGAGGATCTTCTGATCT 540
DB 493 GTGAGGCTTAAGAAGCTTCCCTCGAGAGGCCAGCTACCTGCCGAGGATCTTCTGATCT 552
QY 541 GGAGAACTAGGCCGAAACTCAGGAACATTTTCTTCGAGATTTGAGATACACCCATCCTG 600
DB 553 GGAGAACTAGGCCGAAACTCAGGAACATTTTCTTCGAGATTTGAGATACACCCATCCTG 612
QY 601 TGTCTCTTTTATTTGCAACAGTGCCTGAACTGAAACAGTGTAAAAATCAAGAAGTA 660
DB 613 TGTCTCTTTTATTTGCAACAGTGCCTGAACTGAAACAGTGTAAAAATCAAGAAGTA 672
QY 661 GAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTTTAAAGTGGAGTCAAGAGTTTTAAAG 720
DB 673 GAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTTTAAAGTGGAGTCAAGAGTTTTAAAG 732
QY 721 AATTCGGCAGTATCCCTCCTCGAACTGGAATGGCTCATCAAAATAAATTTAGATATTTG 780
DB 733 AATTCGGCAGTATCCCTCCTCGAACTGGAATGGCTCATCAATAAATTTAGATATTTG 792
QY 781 TCAAGAGTGGTTTTTGAAGAAAAGACCTCTCTTCCAGACAGTGTAGTCGCGACAGAT 840
DB 793 TCAAGAGTGGTTTTTGAAGAAAAGACCTCTCTTCCAGACAGTGTAGTCGCGACAGAT 852

QY 841 TCACACATACAGATGCTGAATGTTTAGGATTTGGGGTGGGGGTTGGAGGCATTGAA 900
DB 853 TCACACATACAGATGCTGAATGTTTAGGATTTGGGGTGGGGGTTGGAGGCATTGAA 912
QY 901 ACAGAAGCAGTTATGCTTGGTCTGCCAGTTTCTTCTACTTTACACAGAGCTGTTGGATCT 960
DB 913 ACAGAAGCAGTTATGCTTGGTCTGCCAGTTTCTTCTACTTTACACAGAGCTGTTGGATCT 972
QY 961 GAGTTAACTGGGTCAATCAAAACCTTTTGTATACATCCATAGATGTTTCTTGGTATTACA 1020
DB 973 GAGTTAACTGGGTCAATCAAAACCTTTTGTATACATCCATAGATGTTTCTTGGTATTACA 1032
QY 1021 AAG 1023
DB 1033 AAG 1035

RESULT 9
US-09-471-275-1719
; Sequence 1719, Application US/09471275
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 782
; CURRENT APPLICATION NUMBER: US 09/471,275
; CURRENT FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: US 09/235,076
; EARLIER FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: US 09/234,611
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: US 09/240,371
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: US 09/277,227
; EARLIER FILING DATE: 1999-03-25
; EARLIER APPLICATION NUMBER: US 09/271,490
; EARLIER FILING DATE: 1999-03-18
; EARLIER APPLICATION NUMBER: US 09/293,972
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 09/274,861
; EARLIER FILING DATE: 1999-03-23
; EARLIER APPLICATION NUMBER: US 60/125,453
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: US 60/126,605
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: US 09/306,350
; EARLIER FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/399,720
; EARLIER FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER: US 09/404,284
; EARLIER FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER:
; EARLIER FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 10451
; SOFTWARE: pt_CT_genes Version 1.0
; SEQ ID NO 1719
; LENGTH: 4194
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (151)...(3040)
; OTHER INFORMATION: similar to g1897827 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
US-09-471-275-1719

Query Match 23.5%; Score 1019.8; DB 18; Length 4194;
Best Local Similarity 99.8%; Pred. No. 2.2e-110;
Matches 1021; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGGAGCCCCCAAGCAGGATACGCTTTGAGTACCTTTATTAACATTAATGACAGT 60
DB 1 ATGGAGCCCCCAAGCAGGATACGCTTTGAGTACCTTTATTAACATTAATGACAGT 60

Db	151	ATGGACGCCCCCAAAACGAGGATACGCCCTTTGAGTACCTTTATTGAACATTTAATGACAGT	210
Qy	61	TCACATAAGAAGTCTCTTCGATGTATCTAAACTTGGCACCAGTATGATCTTGCCTTAC	120
Db	211	TCACATAAGAAGTCTCTTCGATGTATCTAAACTTGGCACCAGTATGATCTTGCCTTAC	270
Qy	121	TCAAATACGGGTCTTTGTTGGAAGCTGCTGTACGAATTTGTGATGCTTTTAAATGAAGAAG	180
Db	271	TCAAATACGGGTCTTTGTTGGAAGCTGCTGTACGAATTTGTGATGCTTTTAAATGAAGAAG	330
Qy	181	GAAGATGTTTATGAACATTTTACAGTGGAAAAACCAAAAGCAATGTTGAAGTGCCTTT	240
Db	331	GAAGATGTTTATGAACATTTTACAGTGGAAAAACCAAAAGCAATGTTGAAGTGCCTTT	390
Qy	241	TTCCCTGCCCGTGTCTTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTTGC	300
Db	391	TTCCCTGCCCGTGTCTTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTTGC	450
Qy	301	GCTATGAGGGAGCGAGTGAAGACTCTTGGAGGTGATCCTGAGAAAGTCCATCTGCTTGT	360
Db	451	GCTATGAGGGAGCGAGTGAAGACTCTTGGAGGTGATCCTGAGAAAGTCCATCTGCTTGT	510
Qy	361	CCGACAGATCTTACAGCTTCACCATCTTTACAAATTGACTTCAGTAAATGTGCAATACAG	420
Db	511	CCGACAGATCTTACAGCTTCACCATCTTTACAAATTGACTTCAGTAAATGTGCAATACAG	570
Qy	421	AATGCACCAATCCTGGAGTGGTGACCTGCAGAAAGCAGAAAGCTCTCTCCACTTAA	480
Db	571	AATGCACCAATCCTGGAGTGGTGACCTGCAGAAAGCAGAAAGCTCTCTCCACTTAA	630
Qy	481	GTGCAGCCTAAGAAGCTTCCCTGCAGAGCCAGACTACCTGCCAGAGATCTGTGATCT	540
Db	631	GTGCAGCCTAAGAAGCTTCCCTGCAGAGCCAGACTACCTGCCAGAGATCTGTGATCT	690
Qy	541	GGAGAACTAGCGCGAAACTCAGGAACATTTCTTCGAGATTGAGAAATACACCCACTCTG	600
Db	691	GGAGAACTAGCGCGAAACTCAGGAACATTTCTTCGAGATTGAGAAATACACCCACTCTG	750
Qy	601	TGTCCTTTTCATTTGCAACCGAGCTGCTGAACCTGAACAGTGTATAAAATCAAGAAGTA	660
Db	751	TGTCCTTTTCATTTGCAACCGAGCTGCTGAACCTGAACAGTGTATAAAATCAAGAAGTA	810
Qy	661	GAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTAAAGTGGAGTCAAGAGTTTTAAAG	720
Db	811	GAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTAAAGTGGAGTCAAGAGTTTTAAAG	870
Qy	721	AATGTGCGAGTGATCCCTCCTGGAACTGGAATGGCTCATCAAAATAACTTAGAATATTG	780
Db	871	AATGTGCGAGGGATCCCTCCTGGAACTGGAATGGCTCATCAAAATAACTTAGAATATTG	930
Qy	781	TCRAGAGTGGTTTTTCAAGAAAAGACCTCCCTTCCAGACAGTGTAGTCGGCACAGAT	840
Db	931	TCRAGAGTGGTTTTTCAAGAAAAGACCTCCCTTCCAGACAGTGTAGTCGGCACAGAT	990
Qy	841	TCACACATAACGATGTGAATGGTTTAGGGATTCTGGGGTGGGGGTTGGAGCAATTGAA	900
Db	991	TCACACATAACGATGTGAATGGTTTAGGGATTCTGGGGTGGGGGTTGGAGCAATTGAA	1050
Qy	901	ACAGAAGCAGTTATGCTTGGTCTGCCAGTTTCTCTTACTTTACAGAGGTGGTGGATGT	960
Db	1051	ACAGAAGCAGTTATGCTTGGTCTGCCAGTTTCTCTTACTTTACAGAGGTGGTGGATGT	1110
Qy	961	GAGTTAACTGGGTTCATCAAAACCTTTTGTATACATCCATAGATGTTGTTCTTGGTATTACA	1020
Db	1111	GAGTTAACTGGGTTCATCAAAACCTTTTGTATACATCCATAGATGTTGTTCTTGGTATTACA	1170
Qy	1021	AAG 1023	
Db	1171	AAG 1173	

RESULT 10

RESOL. IV
US-09-496-914A-7145

```

; Sequence 7145, Application US/09496914A
; GENERAL INFORMATION:
; APPLICANT: Tang, Yuanhua T.
; APPLICANT: Tillinghast, John
; APPLICANT: Sinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 787
; CURRENT APPLICATION NUMBER: US/09/496,914A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/353,690
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/331,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/431,517
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: US 09/328,351
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: US 09/332,782
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: US 09/346,956
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: US 09/362,510
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 09/240,371
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: US 09/248,797
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 09/271,490
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 09/293,972
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 09/274,861
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/125,453
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: US 60/126,605
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/306,350
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/399,720
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/404,284
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/465,877
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: NOT YET ASSIGNED
; PRIOR FILING DATE: 1999-01-19
; NUMBER OF SEQ ID NOS: 10410
; SOFTWARE: plCT_genes Version 1.02
; SEQ ID NO 7145
; LENGTH: 4194
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (151)...(3040)
; OTHER INFORMATION: similar to g1897827 in
; OTHER INFORMATION: Run with FASTXY 3.3t00,
; US-09-496-914A-7145

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Query Match		23.5%;	Score 1019.8;	DB 18;	Length 4194;
Best Local Similarity		99.8%;	Pred. No. 2.2e-110;		
Matches 1021;		Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	ATGGACGCCCAAGCAGATAGCCCTTTGAGTACCTTATTGAAACATTAATGACAGT	60		
Db	151	ATGGACGCCCAAGCAGATAGCCCTTTGAGTACCTTATTGAAACATTAATGACAGT	210		
Qy	61	TCACATAAGAAGTCTTCGATGATCTAAACTTGGCCACCAAGTATGATGTTCTGCCTTAC	120		
Db	211	TCACATAAGAAGTCTTCGATGATCTAAACTTGGCCACCAAGTATGATGTTCTGCCTTAC	270		
Qy	121	TCAATACGGGCTCTTGTGGAGCTGCTGTACGAAATTTGTGATGGCTTTTAAATGAAGAAG	180		
Db	271	TCAATACGGGCTCTTGTGGAGCTGCTGTACGAAATTTGTGATGGCTTTTAAATGAAGAAG	330		
Qy	181	GAAGATGTTATGAACATTTAGACTGGAAACCAACAAAGCAATGTTGAAGTGCCCTTT	240		
Db	331	GAAGATGTTATGAACATTTAGACTGGAAACCAACAAAGCAATGTTGAAGTGCCCTTT	390		
Qy	241	TTCCCTGCCCTGTTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTTGTCT	300		
Db	391	TTCCCTGCCCTGTTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTTGTCT	450		
Qy	301	GCTATGAGGGAGGCGAGTCAAAACTCTTGGAGGTGATCCTGAGAAAGTCCATCCTGCTGT	360		
Db	451	GCTATGAGGGAGGCGAGTCAAAACTCTTGGAGGTGATCCTGAGAAAGTCCATCCTGCTGT	510		
Qy	361	CCGACAGATCTTACAGTTCACAGTTTACCAATTTGACTTCCAGTAACCAAGTTCGATTTGCT	420		
Db	511	CCGACAGATCTTACAGTTCACAGTTTACCAATTTGACTTCCAGTAACCAAGTTCGATTTGCT	480		
Qy	421	ATGACACCAAAATCCTGGAGGTGGTACCTGCGAGAGCCAGACTACCTGCCGAGGATCTTGTATCT	540		
Db	571	ATGACACCAAAATCCTGGAGGTGGTACCTGCGAGAGCCAGACTACCTGCCGAGGATCTTGTATCT	600		
Qy	541	GGAGAACTAGGCCGAAACCTCAGGAGGCTTCAAGTGGAGTTTCAAGAGTTTAAAG	600		
Db	601	GGAGAACTAGGCCGAAACCTCAGGAGGCTTCAAGTGGAGTTTCAAGAGTTTAAAG	660		
Qy	661	GAATTCGGCAGAAATCGAGAGAGGCTTCAAGTGGAGTTTCAAGAGTTTAAAG	720		
Db	721	GAATTCGGCAGAAATCGAGAGAGGCTTCAAGTGGAGTTTCAAGAGTTTAAAG	780		
Qy	781	TCAAGATGGTCTTGAAGAAAGAGCTCCTCTCTCCAGACAGTGTAGTGGCAGACAGAT	840		
Db	841	TCAAGATGGTCTTGAAGAAAGAGCTCCTCTCTCCAGACAGTGTAGTGGCAGACAGAT	900		
Qy	901	ACAGAACAGTATGCTTGGTCTGCCAGTTTCTCTTACTTTACAGAGGTGGTGGATGT	960		
Db	961	GAGTTAACTGGTCTATCAAAACCTTTTGTACATCCATAGATGTTGTTCTTGTATATACA	1020		
Qy	1021	AAG 1023	600		

Db	1171	AAG 1173	0;
RESULT 11			
US-09-560-875A-7145			
; Sequence 7145, Application US/09560875A			
; GENERAL INFORMATION:			
; APPLICANT: Tang Yuanhua T.			
; APPLICANT: Tillingnast, John			
; APPLICANT: Sinku, Ankura			
; APPLICANT: Liu, Chenghua			
; APPLICANT: Drmanac, Radoje T.			
; TITLE OF INVENTION: Novel Contigs Obtained			
; FILE REFERENCE: 787			
; CURRENT APPLICATION NUMBER: US/09/560,875A			
; CURRENT FILING DATE: 2000-04-27			
; Prior application data removed - consult PALM or file wrapper			
; NUMBER OF SEQ ID NOS: 10410			
; SOFTWARE: pt_CT_genes Version 1.02			
; SEQ ID NO 7145			
; LENGTH: 4194			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc.feature			
; LOCATION: (151)...(3040)			
; OTHER INFORMATION: Similar to gi897827 in the genepept database release 114,			
; OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters			
US-09-560-875A-7145			
Query Match			
Best Local Similarity 23.5%; Score 1019.8; DB 22; Length 4194;			
Matches 1021; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Qy	1	ATGGACGCCCAAGCAGATAGCCCTTTGAGTACCTTATTGAAACATTAATGACAGT	60
Db	151	ATGGACGCCCAAGCAGATAGCCCTTTGAGTACCTTATTGAAACATTAATGACAGT	210
Qy	61	TCACATAAGAAGTCTTCGATGATCTAAACTTGGCCACCAAGTATGATGTTCTGCCTTAC	120
Db	211	TCACATAAGAAGTCTTCGATGATCTAAACTTGGCCACCAAGTATGATGTTCTGCCTTAC	270
Qy	121	TCAATACGGGCTCTTGTGGAGCTGCTGTACGAAATTTGTGATGGCTTTTAAATGAAGAAG	180
Db	271	TCAATACGGGCTCTTGTGGAGCTGCTGTACGAAATTTGTGATGGCTTTTAAATGAAGAAG	330
Qy	181	GAAGATGTTATGAACATTTTAGACTGGAAACCAACAAAGCAATGTTGAAGTGCCCTTT	240
Db	331	GAAGATGTTATGAACATTTTAGACTGGAAACCAACAAAGCAATGTTGAAGTGCCCTTT	390
Qy	241	TTCCCTGCCCTGTTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTTGTCT	300
Db	391	TTCCCTGCCCTGTTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTTGTCT	450
Qy	301	GCTATGAGGGAGGCGAGTCAAAACTCTTGGAGGTGATCCTGAGAAAGTCCATCCTGCTGT	360
Db	451	GCTATGAGGGAGGCGAGTCAAAACTCTTGGAGGTGATCCTGAGAAAGTCCATCCTGCTGT	510
Qy	361	CCGACAGATCTTACAGTTCACAGTTTACCAATTTGACTTCCAGTAACCAAGTTCGATTTGCT	420
Db	511	CCGACAGATCTTACAGTTCACAGTTTACCAATTTGACTTCCAGTAACCAAGTTCGATTTGCT	570
Qy	421	ATGACACCAAAATCCTGGAGGTGGTACCTGCGAGAGCCAGACTACCTGCCGAGGATCTTGTATCT	480
Db	571	ATGACACCAAAATCCTGGAGGTGGTACCTGCGAGAGCCAGACTACCTGCCGAGGATCTTGTATCT	630
Qy	481	GTGACACCTAAGAGCTTCCCTGAGAGGCTTCAAGTGGAGTTTCAAGAGTTTAAAG	540
Db	631	GTGACACCTAAGAGCTTCCCTGAGAGGCTTCAAGTGGAGTTTCAAGAGTTTAAAG	600
Qy	541	GGAGAACTAGGCCGAAACCTCAGGAGGCTTCAAGTGGAGTTTCAAGAGTTTAAAG	600
Db	601	GGAGAACTAGGCCGAAACCTCAGGAGGCTTCAAGTGGAGTTTCAAGAGTTTAAAG	660
Qy	661	GAATTCGGCAGAAATCGAGAGAGGCTTCAAGTGGAGTTTCAAGAGTTTAAAG	720
Db	721	GAATTCGGCAGAAATCGAGAGAGGCTTCAAGTGGAGTTTCAAGAGTTTAAAG	780
Qy	781	TCAAGATGGTCTTGAAGAAAGAGCTCCTCTCTCCAGACAGTGTAGTGGCAGACAGAT	840
Db	841	TCAAGATGGTCTTGAAGAAAGAGCTCCTCTCTCCAGACAGTGTAGTGGCAGACAGAT	900
Qy	901	ACAGAACAGTATGCTTGGTCTGCCAGTTTCTCTTACTTTACAGAGGTGGTGGATGT	960
Db	961	GAGTTAACTGGTCTATCAAAACCTTTTGTACATCCATAGATGTTGTTCTTGTATATACA	1020
Qy	1021	AAG 1023	600


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Db 691 GGAGAACTAGCCGAAACTCAGGAACATTTCTTCGAGATTGAGAAATACACCCTCTG 750
Qy 601 TGTCTCTTTTCAATTTGCAACAGTGCCTGAACTCGAAACAGTGTAAAAAATCAAGAAGTA 660
Db 751 TGTCTCTTTTCAATTTGCAACAGTGCCTGAAACAGTGTAAAAAATCAAGAAGTA 810
Qy 661 GAATTCGSCAGAAATCGAGAGAGCTTCAGTCTTTTAAAGTGGAGTTCAAGAGTTTAAAG 720
Db 811 GAATTCGSCAGAAATCGAGAGAGCTTCAGTCTTTTAAAGTGGAGTTCAAGAGTTTAAAG 870
Qy 721 AATGTCGAGTATCCCTCTCGAACTGGAATGGCTCATCAATAAATCTAGATAATTTG 780
Db 871 AATGTCGAGGATCCCTCTCGAACTGGAATGGCTCATCAATAAATCTAGATAATTTG 930
Qy 781 TCAGAGTGGTTTTTGAAGAAAGACCTCTCTTCCACACAGCTGAGTCGGCACAGAT 840
Db 931 TCAGAGTGGTTTTTGAAGAAAGACCTCTCTTCCACACAGCTGAGTCGGCACAGAT 990
Qy 841 TCACACATAAGCATGCTGAAATGTTAGGATTCCTGGGTTGGGGTGGGGTGGGGTGGAA 1050
Db 991 TCACACATAAGCATGCTGAAATGTTAGGATTCCTGGGTTGGGGTGGGGTGGGGTGGAA 1050
Qy 901 ACAGAACAGTATGCTTGGTCTCCAGTCTCTTACTTTACAGAGTGGTGGATGT 960
Db 1051 ACAGAACAGTATGCTTGGTCTCCAGTCTCTTACTTTACAGAGTGGTGGATGT 1110
Qy 961 GAGTTAACTGGTGCATCAAAACCTTTTGTACATCCATAGATGTTCTTGGTATTACA 1020
Db 1111 GAGTTAACTGGTGCATCAAAACCTTTTGTACATCCATAGATGTTCTTGGTATTACA 1170
Qy 1021 AAG 1023
Db 1171 AAG 1173
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RESULT 12

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US-60-324-185-26664
; Sequence 26664, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preethi
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 26664
; LENGTH: 4729
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 384853.9
; NAME/KEY: unsure
; LOCATION: 1279
; OTHER INFORMATION: a, t, c, g, or other
US-60-324-185-26664
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Query Match 23.5%; Score 1019.8; DB 76; Length 4729;
Best Local Similarity 99.8%; Pred. No. 2.2e-110;
Matches 1021; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 ATGGACGCCCAAGCAGGATACGCCCTTTGAGTACCTTTATGAAACATTAAATGACAGT 60
Db 131 ATGGACGCCCAAGCAGGATACGCCCTTTGAGTACCTTTATGAAACATTAAATGACAGT 190
Qy 61 TCACATAAGAAGTCTTCGATGTATCAAACTTGGCACCAGATGATGTTCTGCTCTTAC 120
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Db 191 TCACATAAGAAGTCTTCGATGTATCTAACTTGGCACCAGATATGATGTTCTGCTCTTAC 250
Qy 121 TCAATACGGGCTCTTGTGTGAAGCTGCTGTACGAAATTTGTGATGGCTTTTAAATGAAGAAG 180
Db 251 TCAATACGGGCTCTTGTGTGAAGCTGCTGTACGAAATTTGTGATGGCTTTTAAATGAAGAAG 310
Qy 181 GAAGATGTTTATGAACATTTTGTGAGTGGAAACCAACAAAGCAATTTGTAAGTGGCCCTTT 240
Db 311 GAAGATGTTTATGAACATTTTGTGAGTGGAAACCAACAAAGCAATTTGTAAGTGGCCCTTT 370
Qy 241 TTCCCTGCCCGTGTCTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTTGGCT 300
Db 371 TTCCCTGCCCGTGTCTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTTGGCT 430
Qy 301 GCTATGAGGAGGAGTGAACCTCTTGGAGTGTCTGAGAAAGTCCATCCTGCTTGT 360
Db 431 GCTATGAGGAGGAGTGAACCTCTTGGAGTGTCTGAGAAAGTCCATCCTGCTTGT 490
Qy 361 CGACAGATCTTTACAGTTGACCATTTCTTTACAAATTTGACTTCAGTAAATGTGCAATACAG 420
Db 491 CGACAGATCTTTACAGTTGACCATTTCTTTACAAATTTGACTTCAGTAAATGTGCAATACAG 550
Qy 421 AATGCACCAAACTCGAGGTGGTGACCTGCAGAAAGCAGGAAAGCTCTCTCCACTTAAA 480
Db 551 AATGCACCAAACTCGAGGTGGTGACCTGCAGAAAGCAGGAAAGCTCTCTCCACTTAAA 610
Qy 481 GTGCAGCCTTAAGAAAGCTTCCCTGCAGAGGCCAGACTTACCTGCCGAGGATCTTGTGATTTCT 540
Db 611 GTGCAGCCTTAAGAAAGCTTCCCTGCAGAGGCCAGACTTACCTGCCGAGGATCTTGTGATTTCT 670
Qy 541 GGAGAACTAGGCGGAAACTCAGGAACATTTTCTGCGAGATTTGAGAAATACACCCATCTCGT 600
Db 671 GGAGAACTAGGCGGAAACTCAGGAACATTTTCTGCGAGATTTGAGAAATACACCCATCTCGT 730
Qy 601 TGTCCCTTTTCAATTTGCAACAGTGGCTGAACCTGAAACAGTGTAAAAAATCAAGAAFTA 660
Db 731 TGTCCCTTTTCAATTTGCAACAGTGGCTGAACCTGAAACAGTGTAAAAAATCAAGAAFTA 790
Qy 661 GAATTCGGCAGAAATCGAGAGAGGCTTCAGTCTTTTAAAGTGGAGTTCAGAGTTTTAAAG 720
Db 791 GAATTCGGCAGAAATCGAGAGAGGCTTCAGTCTTTTAAAGTGGAGTTCAGAGTTTTAAAG 850
Qy 721 AATGTCGAGTATCCCTCTCGAACTGGAATGGCTCATCAATAAATCTAGATAATTTG 780
Db 851 AATGTCGAGTATCCCTCTCGAACTGGAATGGCTCATCAATAAATCTAGATAATTTG 910
Qy 781 TCAAGAGTGGTTTTTGAAGAAAGACCTCTCTTCCACAGACAGTGTAGTCGGCACAGAT 840
Db 911 TCAAGAGTGGTTTTTGAAGAAAGACCTCTCTTCCACAGACAGTGTAGTCGGCACAGAT 970
Qy 841 TCACACATAAGCATGTTGTAATGGTGTAGGATTTCTGGGTTGGGGTGGGGTGGAGGCATTGAA 900
Db 971 TCACACATAAGCATGTTGTAATGGTGTAGGATTTCTGGGTTGGGGTGGGGTGGAGGCATTGAA 1030
Qy 901 ACAGAACAGTATGCTTGGTGTGCGAGTCTCTTACTTTTACCAGAGTGGTTCGATGT 960
Db 1031 ACAGAACAGTATGCTTGGTGTGCGAGTCTCTTACTTTTACCAGAGTGGTTCGATGT 1090
Qy 961 GAGTTAACTGGGTCATCAAAACCTTTTGTACATCCATAGATGTTGTTCTTCTGTTATACA 1020
Db 1091 GAGTTAACTGGGTCATCAAAACCTTTTGTACATCCATAGATGTTGTTCTTCTGTTATACA 1150
Qy 1021 AAG 1023
Db 1151 AAG 1153
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RESULT 13
US-60-339-453-290
; Sequence 290, Application us/60339453
; GENERAL INFORMATION:
; APPLICANT: Wang, Y. Tom
; APPLICANT: Wang, Zhiwei

APPLICANT: Wang, Jian-Rui
APPLICANT: Ghosh, Malabika
APPLICANT: Weng, Gezhi
APPLICANT: Boyle, Bryan J
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids and
FILE OF INVENTION: Polypeptides
FILE REFERENCE: 812
CURRENT APPLICATION NUMBER: US/60/339,453
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: PCT/US01/03800
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: US 09/577,409
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: PCT/US01/04927
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: PCT/US01/04941
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 09/552,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/770,160
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: PCT/US01/08656
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 412
SOFTWARE: pc_FL_genes Version 6.0
SEQ ID NO 290

Query Match 23.5%; Score 1019.8; DB 77; Length 4871;
Best Local Similarity 99.8%; Pred. No. 2.1e-110;
Matches 1021; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGAGCCCCAAAAGCAGGATACGCTTTGAGTACCTTTATGAACATTAATGACAGT 60
DB 151 ATGGAGCCCCAAAAGCAGGATACGCTTTGAGTACCTTTATGAACATTAATGACAGT 210
QY 61 TCACATAAAGAGTCTTCGATGATATCTAAACCTGGCACCAGTATGATGTTCTGCCTTAC 120
DB 211 TCACATAAAGAGTCTTCGATGATATCTAAACCTGGCACCAGTATGATGTTCTGCCTTAC 270
QY 121 TCAATACGGGCTCTGTTGGAAGCTCTGTACGAAATGATGCTGCTTTTAAATGAAGAAG 180
DB 271 TCAATACGGGCTCTGTTGGAAGCTCTGTACGAAATGATGCTGCTTTTAAATGAAGAAG 330

QY 181 GAAGATGTTATGAACATTTTAGACTGGAAACCAAAAGCAATGTTGAAGTGCCTTT 240
DB 331 GAAGATGTTATGAACATTTTAGACTGGAAACCAAAAGCAATGTTGAAGTGCCTTT 390
QY 241 TTCCCTGCCCGTGTCTTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTGCT 300
DB 391 TTCCCTGCCCGTGTCTTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTGCT 450
QY 301 GCTATGAGGGAGGAGCAGTGAACACTCTTTGGAGGTGATCCTCAGAAAGTCCATCTGCTTGT 360
DB 451 GCTATGAGGGAGGAGCAGTGAACACTCTTTGGAGGTGATCCTCAGAAAGTCCATCTGCTTGT 510
QY 361 CCGACAGATCTTACAGTTGACCATTTTACAAATTCAGTAAATGTGCAATACAG 420
DB 511 CCGACAGATCTTACAGTTGACCATTTTACAAATTCAGTAAATGTGCAATACAG 570
QY 421 AATGCACCAATCTCGAGGTGACCTGCAGAAAGCAGAAAGCTCTCTCCACTTAA 480
DB 571 AATGCACCAATCTCGAGGTGACCTGCAGAAAGCAGAAAGCTCTCTCCACTTAA 630
QY 481 GTGCAGCCTAAGAGCTTCCCTGCAGAGCCAGACTACCTGCCGAGGATCTTGTGATTCT 540
DB 631 GTGCAGCCTAAGAGCTTCCCTGCAGAGCCAGACTACCTGCCGAGGATCTTGTGATTCT 690
QY 541 GGAGAACTAGCCGAAACTCAGGAACATTTTCTTCGAGATTTGAGAAATACACCATCTG 600
DB 691 GGAGAACTAGCCGAAACTCAGGAACATTTTCTTCGAGATTTGAGAAATACACCATCTG 750
QY 601 TGTCTTTTTCATTTGCAACCCAGTGCCTGAACCTGAAACAGTGTAAAAATCAAGAGTA 660
DB 751 TGTCTTTTTCATTTGCAACCCAGTGCCTGAACCTGAAACAGTGTAAAAATCAAGAGTA 810
QY 661 GAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTAAAGTGGAGTTCAAGAGTTTTAAAG 720
DB 811 GAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTAAAGTGGAGTTCAAGAGTTTTAAAG 870
QY 721 AATGTGGCAGTGTCCCTCTCGAACTGGAATGGCTCATCAATAACTTAGAATATTG 780
DB 871 AATGTGGCAGGATCCCTCTCGAACTGGAATGGCTCATCAATAACTTAGAATATTG 930
QY 781 TCAAGAGTGTGTTTGAAGAAAAGACCTCTCTTCCACACAGCTGTAGTCGCACAGAT 840
DB 931 TCAAGAGTGTGTTTGAAGAAAAGACCTCTCTTCCACACAGCTGTAGTCGCACAGAT 990
QY 841 TCACATAACAGTGTGAATGTTTGAAGATTCCTGGGTGGGGGTGGAGGCAATGAA 900
DB 991 TCACATAACAGTGTGAATGTTTGAAGATTCCTGGGTGGGGGTGGAGGCAATGAA 1050
QY 901 ACAGAAGCAGTTATGCTTGGTCTGCCAGTTTCTCTTACTTTACAGAGGTGGTGGATGT 960
DB 1051 ACAGAAGCAGTTATGCTTGGTCTGCCAGTTTCTCTTACTTTACAGAGGTGGTGGATGT 1110
QY 961 GAGTTAACTGGTTCATCAAAACCCCTTTGTTTACATCCATAGATGTTGTTCTGGTATTACA 1020
DB 1111 GAGTTAACTGGTTCATCAAAACCCCTTTGTTTACATCCATAGATGTTGTTCTGGTATTACA 1170
QY 1021 AAG 1023
DB 1171 AAG 1173

RESULT 14
US-60-339-453-63
; Sequence 63, Application US/60339453
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Weng, Gezhi
; APPLICANT: Boyle, Bryan J
; APPLICANT: Drmanac, Radoje T

; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 812
; CURRENT APPLICATION NUMBER: US/60/339,453
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/577,409
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: PCT/US01/04927
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: PCT/US01/04941
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/770,160
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/US01/08656
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 63
; LENGTH: 5034.
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76)..(3282)
; US-60-339-453-63

Query Match 23.1%; Score 1004; DB 77; Length 5034;
Best Local Similarity 100.0%; Pred. No. 1.5e-108;
Matches 1004; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 GATACGCCCTTTCAGTACCTTATTGAACATTAATGACAGTTCACATGAAGTCTTCG 79
Db 410 GATACGCCCTTTCAGTACCTTATTGAACATTAATGACAGTTCACATGAAGTCTTCG 469
Qy 80 ATGTATCTAACTTGGCACCAAGTATGTTCTGCTTACTCAATACGGGTCTGTTGG 139
Db 470 ATGTATCTAACTTGGCACCAAGTATGTTCTGCTTACTCAATACGGGTCTGTTGG 529
Qy 140 AAGTGTCTAGCAAAATGTTGATGCTTTTAAATGAAGAAGAGATGTTATGAACATTT 199
Db 530 AAGTGTCTAGCAAAATGTTGATGCTTTTAAATGAAGAAGAGATGTTATGAACATTT 589
Qy 200 TAGACTGGAAACCAACCAACCAATGTTGAAGTCCCTTTTCCCTGCCCGTGTCTTC 259

Db 590 TAGACTGGAAACCAACCAACCAATGTTGAAGTCCCTTTTCCCTGCCCGTGTCTTC 649
Qy 260 TTCAAGATTTTACTGGAATACCAGCAATGTTGGATTTTGTCTGCTATGAGGAGGCACTGA 319
Db 650 TTCAAGATTTTACTGGAATACCAGCAATGTTGGATTTTGTCTGCTATGAGGAGGCACTGA 709
Qy 320 AAACCTTTGGAGGTGATCCTCGAGAAAGTCCATCCTGCTTGTCCGACAGATCTTACAGTTG 379
Db 710 AAACCTTTGGAGGTGATCCTCGAGAAAGTCCATCCTGCTTGTCCGACAGATCTTACAGTTG 769
Qy 380 ACCATCTTTTACAAATTCAGTTCAAGTAAATGTCGAATACAGATGACCAAAATCCTGGAG 439
Db 770 ACCATCTTTTACAAATTCAGTTCAAGTAAATGTCGAATACAGATGACCAAAATCCTGGAG 829
Qy 440 GTGCTGACCTGCAGAAAGCAGGAAAGCTCTCCACCTTAAAGTGCAGCCTTAAAGAAGCTTC 499
Db 830 GTGCTGACCTGCAGAAAGCAGGAAAGCTCTCCACCTTAAAGTGCAGCCTTAAAGAAGCTTC 889
Qy 500 CCTGCAGAGGCCAGACTACCTGCCGAGGATCTTGTGATTTCTGGAGAACTAGGCCGAAACT 559
Db 890 CCTGCAGAGGCCAGACTACCTGCCGAGGATCTTGTGATTTCTGGAGAACTAGGCCGAAACT 949
Qy 560 CAGGAACATTTTCTTCGAGATTCAGAAATACACCCATCCTGTCTCTTTTTCATTTCGCAAC 619
Db 950 CAGGAACATTTTCTTCGAGATTCAGAAATACACCCATCCTGTCTCTTTTTCATTTCGCAAC 1009
Qy 620 CAGTCCCTGAAACCTGAAACAGTGTAAATAATCAAGAAAGTAGAATTCGGCAGAAATCGAG 679
Db 1010 CAGTCCCTGAAACCTGAAACAGTGTAAATAATCAAGAAAGTAGAATTCGGCAGAAATCGAG 1069
Qy 680 AGAGGCTTCAGTTTTTAAAGTGGAGTTCAAGAGTTTTTAAAGAATTTGAGAGTGTATGAG 739
Db 1070 AGAGGCTTCAGTTTTTAAAGTGGAGTTCAAGAGTTTTTAAAGAATTTGAGAGTGTATGAG 1129
Qy 740 CTGGAACCTGGAATGGCTCATCAATAAATAGAAATTTGTCAGAGTGGTTTTTGAAG 799
Db 1130 CTGGAACCTGGAATGGCTCATCAATAAATAGAAATTTGTCAGAGTGGTTTTTGAAG 1189
Qy 800 AAAAGACCTCCTCTTCCAGACAGTGTAGTCCGACAGATTCACACATACAGATGGTGA 859
Db 1190 AAAAGACCTCCTCTTCCAGACAGTGTAGTCCGACAGATTCACACATACAGATGGTGA 1249
Qy 860 ATGTTTATGAGGATTCCTGGGTGGGGGTGGAGGCAATTGAAAGAGAGTGTATGAGTTG 919
Db 1250 ATGTTTATGAGGATTCCTGGGTGGGGGTGGAGGCAATTGAAAGAGAGTGTATGAGTTG 1309
Qy 920 GTCTGCCAGTTTCTCTTACTTTACCAGAGTGGTTGGATGTGAGTTAACTGGGTATCAA 979
Db 1310 GTCTGCCAGTTTCTCTTACTTTACCAGAGTGGTTGGATGTGAGTTAACTGGGTATCAA 1369
Qy 980 ACCCTTTTGTATCATCCATAGATGTTCTTCTTGTGTTATACAAAG 1023
Db 1370 ACCCTTTTGTATCATCCATAGATGTTCTTCTTGTGTTATACAAAG 1413

RESULT 15
US-09-924-396B-17
; Sequence 17. Application US/09924396B
; GENERAL INFORMATION:
; APPLICANT: Kirsch, Wolff
; APPLICANT: Lennart, Anton
; APPLICANT: Kellin, Wayne
; APPLICANT: Kang, Dae-Kyung
; APPLICANT: Levine, Rodney
; APPLICANT: Rouault, Tracey
; TITLE OF INVENTION: IRON-REGULATING PROTEIN-2 (IRP-2) IS
; FILE REFERENCE: LOMAU.140A
; CURRENT APPLICATION NUMBER: US/09/924,396B
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/222,863
; PRIOR FILING DATE: 2000-08-04

; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 2867
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-924-396B-17

Query Match 22.8%; Score 990; DB 34; Length 2867;

Best Local Similarity 100.0%; Pred. No. 7e-107;

Matches 990; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	34	TACCTTATGAAACATTAATGACAGTTCACATAAGAGTCTTCGATGTATCTAAACTT	93
DB	1	TACCTTATGAAACATTAATGACAGTTCACATAAGAGTCTTCGATGTATCTAAACTT	60
QY	94	GGCACCAAGTATGATGTTCTGCTTACTCAATACGGGTCTGTGGAAGTGTGTACGA	153
DB	61	GGCACCAAGTATGATGTTCTGCTTACTCAATACGGGTCTGTGGAAGTGTGTACGA	120
QY	154	AATGTGATGGCTTTTAAATGAAGAGGAGATCTTATGAACATTTTAGACTGGAAC	213
DB	121	AATGTGATGGCTTTTAAATGAAGAGGAGATCTTATGAACATTTTAGACTGGAAC	180
QY	214	AAACAAGCAATGTTGAAGTGCCTTTTCCCTGCGGTCTCTCTCAAGATTTTACT	273
DB	181	AAACAAGCAATGTTGAAGTGCCTTTTCCCTGCGGTCTCTCTCAAGATTTTACT	240
QY	274	GAATACCAAGCAATGTTGATTTTCTGCTATGAGGAGGAGTGAACCTCTTGGAGT	333
DB	241	GAATACCAAGCAATGTTGATTTTCTGCTATGAGGAGGAGTGAACCTCTTGGAGT	300
QY	334	GATCCTGAGAAAGTCCATCCTGCTGTCGACAGATCTTACAGTTGACCATTTTACAA	393
DB	301	GATCCTGAGAAAGTCCATCCTGCTGTCGACAGATCTTACAGTTGACCATTTTACAA	360
QY	394	ATTGACTTCAGTAAATGTGCAATACAGAAATGCACCAATCCTGGAGGTGTGACCTGCAG	453
DB	361	ATTGACTTCAGTAAATGTGCAATACAGAAATGCACCAATCCTGGAGGTGTGACCTGCAG	420
QY	454	AAAGCAGGAAGCTCTCCACTTAAAGTGCAGCCTTAGAGCTTCCCTGCAGAGGCCAG	513
DB	421	AAAGCAGGAAGCTCTCCACTTAAAGTGCAGCCTTAGAGCTTCCCTGCAGAGGCCAG	480
QY	514	ACTACCTGCCGAGGATCTGTGATCTCGAGAACTAGGCCGAAACTCAGGAACATTTTCT	573
DB	481	ACTACCTGCCGAGGATCTGTGATCTCGAGAACTAGGCCGAAACTCAGGAACATTTTCT	540
QY	574	TGCGAGATTGAGAAATACACCCATCCTGTGCTCTTTTCATTTGCAACCAAGTCCCTGAACCT	633
DB	541	TGCGAGATTGAGAAATACACCCATCCTGTGCTCTTTTCATTTGCAACCAAGTCCCTGAACCT	600
QY	634	GAACAGTGTAAAAAATCAAGAGTAAATTCGCGAGAAATCGAGAGAGGCTTCAGTTT	693
DB	601	GAACAGTGTAAAAAATCAAGAGTAAATTCGCGAGAAATCGAGAGAGGCTTCAGTTT	660
QY	694	TTTAAGTGGAGTCAAGAGTTTAAAGAAATGCGCAGTATCCCTCTCGAACTGGAATG	753
DB	661	TTTAAGTGGAGTCAAGAGTTTAAAGAAATGCGCAGTATCCCTCTCGAACTGGAATG	720
QY	754	GCTCATCAATAAATAGATATTTGTCAAGAGTGGTTTTGAAGAAAAAGACCTCCTC	813
DB	721	GCTCATCAATAAATAGATATTTGTCAAGAGTGGTTTTGAAGAAAAAGACCTCCTC	780
QY	814	TTCCACAGACAGTGTAGTGGCAGAGATTCACACATAACGATGGTGAATGTTTAGGAT	873
DB	781	TTCCACAGACAGTGTAGTGGCAGAGATTCACACATAACGATGGTGAATGTTTAGGAT	840
QY	874	CTGGGTGGGGGTTGGAGGCATTCAACAGAGCAGTATGCTTGGTCTGCCAGTTTCT	933
DB	841	CTGGGTGGGGGTTGGAGGCATTCAACAGAGCAGTATGCTTGGTCTGCCAGTTTCT	900
QY	934	CTTACTTTTACCAGAGGTGGTGGATGTGAGTTAACTGGGTCAATCAAAACCTTTTGTAC	993

Db	901	CTTACTTTACCAGAGGTGGTGGATGTGAGTTAACTGGTCAATCAAAACCTTTTGTAC	960
QY	994	TCCATAGATGTTGTTCTTGGTATTACAAAG	1023
DB	961	TCCATAGATGTTGTTCTTGGTATTACAAAG	990

Search completed: February 28, 2003, 11:44:35
Job time : 9172 secs

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OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 04:09:08 ; Search time 983 Seconds
(without alignments)
7528.540 Million cell updates/sec

Title: US-09-730-559B-7

Perfect score: 4343

Sequence: 1 atggagcgcacaaagcagg.....attcacagcagtcctctct 4343

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3936061 seqs, 852009584 residues

Total number of hits satisfying chosen parameters: 7872122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_New.*

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2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
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6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1023	23.6	2821	5	US-09-724-676-1037
2	1023	23.6	2821	5	US-09-724-676-1037
3	877.2	20.2	3770	6	US-10-338-044-2158
4	877.2	20.2	3770	7	US-60-436-643-4106
5	654.8	15.1	5601	6	US-10-144-771-5266
6	368	8.5	47684	5	US-09-949-004-699
C 7	356.6	8.2	114693	1	PCT-US02-09734-3
C 8	336.4	7.7	235033	6	US-10-301-844-1
C 9	336.4	7.7	237326	6	US-10-301-844-1
C 10	325.8	7.5	4384464	5	US-09-948-124-7
C 11	317.4	7.3	465237	1	PCT-US02-25201A-1
C 12	315.6	7.3	14277	7	US-60-427-045-313
C 13	313.8	7.2	267482	5	US-09-949-002-659
C 14	313.8	7.2	267505	5	US-09-949-002-783
C 15	312.6	7.2	859705	5	US-09-948-124-60
C 16	310	7.1	177528	7	US-60-449-629-846
C 17	309.8	7.1	52174	5	US-09-949-002-573
C 18	309.8	7.1	52289	5	US-09-949-002-720
C 19	309.2	7.1	86624	1	PCT-US02-36095-1
C 20	309.2	7.1	63824	1	PCT-US02-34679-347
C 21	309.2	7.1	63824	1	PCT-US02-34679-348
C 22	309.2	7.1	63824	6	US-10-282-174-347
C 23	309.2	7.1	63824	6	US-10-282-174-348
C 24	308.8	7.1	128034	1	PCT-US02-34679-186
C 25	308.8	7.1	128034	1	PCT-US02-34679-187
C 26	308.8	7.1	128034	6	US-10-282-174-186

C 27	308.8	7.1	128034	6	US-10-282-174-187	Sequence 187, App
C 28	308.8	7.1	202100	1	PCT-US02-34679-484	Sequence 484, App
C 29	308.8	7.1	202100	6	US-10-282-174-484	Sequence 484, App
C 30	308.6	7.1	260209	6	US-10-025-966A-23	Sequence 23, Appl
C 31	308.6	7.1	260209	6	US-10-265-071-23	Sequence 23, Appl
C 32	308	7.1	202100	1	PCT-US02-34679-484	Sequence 484, App
C 33	308	7.1	202100	6	US-10-282-174-484	Sequence 484, App
C 34	307.6	7.1	276820	1	PCT-US02-32700-9	Sequence 9, Appl
C 35	307.6	7.1	276820	6	US-10-271-416-9	Sequence 9, Appl
C 36	307	7.1	110096	7	US-60-423-586-68	Sequence 68, Appl
C 37	307	7.1	110096	7	US-60-427-194-68	Sequence 68, Appl
C 38	306.4	7.1	61108	5	US-09-949-002-608	Sequence 608, App
C 39	306.2	7.1	35357	5	US-09-783-130A-3	Sequence 3, Appl
C 40	306	7.0	457679	5	US-09-948-124-120	Sequence 120, App
C 41	306	7.0	4384454	5	US-09-948-124-7	Sequence 7, Appl
C 42	305.4	7.0	9451	6	US-10-243-475-131	Sequence 131, App
C 43	305.2	7.0	19793	1	PCT-US02-40718-30	Sequence 30, Appl
C 44	305	7.0	137870	6	US-10-351-951-1	Sequence 1, Appl
C 45	304.8	7.0	601	5	US-09-949-004-717	Sequence 717, App

ALIGNMENTS

RESULT 1

US-09-724-676-1037
; Sequence 1037, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 125181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1037
; LENGTH: 2821
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-1037

Query Match 23.6%; Score 1023; DB 5; Length 2821;
Best Local Similarity 100.0%; Pred. No. 1.6e-114;
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGAGCGCCCAAGCAGGATACGCCCTTGGAGTACCTTATTGAAACATTAATGACAGT	60
DB	13	ATGGAGCGCCCAAGCAGGATACGCCCTTGGAGTACCTTATTGAAACATTAATGACAGT	72
QY	61	TCACATAAGAAGTCTTCGATGATCTAACTTGCACCAAGATGATGTTCTGCCTTAC	120
DB	73	TCACATAAGAAGTCTTCGATGATCTAACTTGCACCAAGATGATGTTCTGCCTTAC	132
QY	121	TCAATACGGGTCTTCTTGGAAAGTCTGTACGAAATCTGATGGCTTTTAAATGAAGAAG	180
DB	133	TCAATACGGGTCTTCTTGGAAAGTCTGTACGAAATCTGATGGCTTTTAAATGAAGAAG	192
QY	181	GAAGATGTTATGAACATTTTATAGCTGGAAACCAACCAACCAATGTTGAAGTGCCTTT	240
DB	193	GAAGATGTTATGAACATTTTATAGCTGGAAACCAACCAACCAATGTTGAAGTGCCTTT	252
QY	241	TTCCCTGCCCGTGTCTTCTTCAAGATTTTACTGCAATACCAAGTGGTGGATTTTGT	300
DB	253	TTCCCTGCCCGTGTCTTCTTCAAGATTTTACTGCAATACCAAGTGGTGGATTTTGT	312
QY	301	GCTATGAGGAGGAGTGAACACTCTTGGAGGTGATCTGAGAAGTCCATCTGCTTGT	360
DB	313	GCTATGAGGAGGAGTGAACACTCTTGGAGGTGATCTGAGAAGTCCATCTGCTTGT	372
QY	361	CCGACAGATCTTACAGTTGACCATTTCTTACAAATGACTTCAGTAATGTCGAATACAG	420
DB	373	CCGACAGATCTTACAGTTGACCATTTCTTACAAATGACTTCAGTAATGTCGAATACAG	432

QY 421 AATGACCAAAATCCCTGGAGTGGTACCTGCAGAAAGCAGGAAAGCTCTCTCCACTTAAA 480
 DB 433 AATGACCAAAATCCCTGGAGTGGTACCTGCAGAAAGCAGGAAAGCTCTCTCCACTTAAA 492
 QY 481 GTGAGCCTTAAGAAGTTCCTTCGAGAGGCCAGACTACTCGCCGAGGATCTTGTGATTTCT 540
 DB 493 GTGAGCCTTAAGAAGTTCCTTCGAGAGGCCAGACTACTCGCCGAGGATCTTGTGATTTCT 552
 QY 541 GGAGAACTAGGCGGAATTCAGAGAACTTCTTCGAGATTCAGAAATACACCCATCTCG 600
 DB 553 GGAGAACTAGGCGGAATTCAGAGAACTTCTTCGAGATTCAGAAATACACCCATCTCG 612
 QY 601 TGTCTCTTTTCATTTGCAACCACTGCTGAACTGAAACAGTCTTAAAAAATCAAGAAGTA 660
 DB 613 TGTCTCTTTTCATTTGCAACCACTGCTGAACTGAAACAGTCTTAAAAAATCAAGAAGTA 672
 QY 661 GAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTAAAGTTCAGAGTTTTTAAAG 720
 DB 673 GAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTAAAGTTCAGAGTTTTTAAAG 732
 QY 721 AATGTGGCAGTATCCCTCTGAACTGGAATGGCTCATCAATAAATCTAGAAATATTG 780
 DB 733 AATGTGGCAGTATCCCTCTGAACTGGAATGGCTCATCAATAAATCTAGAAATATTG 792
 QY 781 TCAAGAGTGGTTTTTGAAGAAAGACCTCTCTTCCAGACAGTGTAGTCGGCAGAT 840
 DB 793 TCAAGAGTGGTTTTTGAAGAAAGACCTCTCTTCCAGACAGTGTAGTCGGCAGAT 852
 QY 841 TCACACATACAGTAAATGGTTTAGGGATTCCTGGGGTGGGGGTTGGAGGCATTTGAA 900
 DB 853 TCACACATACAGTAAATGGTTTAGGGATTCCTGGGGTGGGGGTTGGAGGCATTTGAA 912
 QY 901 ACAGAGCAGTATGCTGCTGCGAGTTCTCTTACTTTTACCAGAGTGGTTGGATGT 960
 DB 913 ACAGAGCAGTATGCTGCTGCGAGTTCTCTTACTTTTACCAGAGTGGTTGGATGT 972
 QY 961 GAGTTAACTGGGTCATCAAAACCCCTTTTGTATACATCCATAGATGTTCTTGGTATTACA 1020
 DB 973 GAGTTAACTGGGTCATCAAAACCCCTTTTGTATACATCCATAGATGTTCTTGGTATTACA 1032
 QY 1021 AAG 1023
 DB 1033 AAG 1035

RESULT 2

US-09-724-676A-1037
 ; Sequence 1037, Application US/09724676A
 ; GENERAL INFORMATION:
 ; APPLICANT: Comugen LTD
 ; TITLE OF INVENTION: Variants of alternative splicing
 ; FILE REFERENCE: 129181.4 Comugen
 ; CURRENT APPLICATION NUMBER: US/09/724, 676A
 ; CURRENT FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 97222
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1037
 ; LENGTH: 2821
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-724-676A-1037

Query Match 23.6%; Score 1023; DB 5; Length 2821;
 Best Local Similarity 100.0%; Pred. No. 1.6e-114;
 Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACGCCCAAGCAGGATACGCTTTGAGTACCTTATTGAAACATTAATGACAGT 60
 DB 13 ATGGACGCCCAAGCAGGATACGCTTTGAGTACCTTATTGAAACATTAATGACAGT 72
 QY 61 TCACATAGAAGTTCCTCGATGTATCTAAACTTGGCACCAGATGATGTTCTGCGCTTAC 120
 DB 73 TCACATAGAAGTTCCTCGATGTATCTAAACTTGGCACCAGATGATGTTCTGCGCTTAC 132

RESULT 3

US-10-338-044-2158
 ; Sequence 2158, Application US/10338044
 ; GENERAL INFORMATION:
 ; APPLICANT: MENDRICK, Donna
 ; APPLICANT: PORTER, Mark
 ; APPLICANT: JOHNSON, Kory

QY 121 TCATACGGGTCTTGTGTGGAAGCTGCTGTACGAAATTTGTGATGGCTTTTAAATGAAGAAG 180
 DB 133 TCATACGGGTCTTGTGTGGAAGCTGCTGTACGAAATTTGTGATGGCTTTTAAATGAAGAAG 192
 QY 181 GAGATCTTATGAACATTTTAGACTGGAAACCAACAAAGCAATCTTGAAGTGCCCTTT 240
 DB 193 GAGATCTTATGAACATTTTAGACTGGAAACCAACAAAGCAATCTTGAAGTGCCCTTT 252
 QY 241 TTCCCTCCCGTGTCTTCTCAAGATTTTACTTGGAAATACCAGCAATGGTGGATTTTGCT 300
 DB 253 TTCCCTCCCGTGTCTTCTCAAGATTTTACTTGGAAATACCAGCAATGGTGGATTTTGCT 312
 QY 301 GCTATGAGGAGGAGTGAACACTTCTTGGAGTGTCTCTGAGAAAGTCCATCTCTGCTTGT 360
 DB 313 GCTATGAGGAGGAGTGAACACTTCTTGGAGTGTCTCTGAGAAAGTCCATCTCTGCTTGT 372
 QY 361 CCGACAGATCTTACAGTTGACCATTTTACAAATTCACATTCAGTAATCTGCAANTACAG 420
 DB 373 CCGACAGATCTTACAGTTGACCATTTTACAAATTCAGTAATTCAGTAATCTGCAANTACAG 432
 QY 421 AATGCACAAATCTCGAGTGTGACCTGCAGAAAGCAGGAAAGCTCTCTCCACTTAAA 480
 DB 433 AATGCACAAATCTCGAGTGTGACCTGCAGAAAGCAGGAAAGCTCTCTCCACTTAAA 492
 QY 481 GTGAGCCTTAAGAAGTTCCTTCGAGAGGCCAGACTACTTGGCCGAGGATCTTGTGATTTCT 540
 DB 493 GTGAGCCTTAAGAAGTTCCTTCGAGAGGCCAGACTACTTGGCCGAGGATCTTGTGATTTCT 552
 QY 541 GGAGAACTAGGCCCAAACTCAGGAACATTTTCTTCGAGATTCAGAAATACACCCATCTG 600
 DB 553 GGAGAACTAGGCCCAAACTCAGGAACATTTTCTTCGAGATTCAGAAATACACCCATCTG 612
 QY 601 TGTCTTTTTCATTTGCAACCACTGCTGAACTGAAACAGTGTAAAAAATCAAGAAGTA 660
 DB 613 TGTCTTTTTCATTTGCAACCACTGCTGAACTGAAACAGTGTAAAAAATCAAGAAGTA 672
 QY 661 GAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTAAAGTTCAGAGTTTTTAAAG 720
 DB 673 GAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTAAAGTTCAGAGTTTTTAAAG 732
 QY 721 AATGTGGCAGTATCCCTCTGAACTGGAATGGCTCATCAATAAATCTAGAAATATTG 780
 DB 733 AATGTGGCAGTATCCCTCTGAACTGGAATGGCTCATCAATAAATCTAGAAATATTG 792
 QY 781 TCAGAGTGGTTTTTGAAGAAAGACCTCTCTTCCAGACAGTGTAGTCGGCAGAT 840
 DB 793 TCAGAGTGGTTTTTGAAGAAAGACCTCTCTTCCAGACAGTGTAGTCGGCAGAT 852
 QY 841 TCACACATACAGTGGTGAATGGTTTAGGGATTCCTGGGGTGGGGGTTGGAGGCATTTGAA 900
 DB 853 TCACACATACAGTGGTGAATGGTTTAGGGATTCCTGGGGTGGGGGTTGGAGGCATTTGAA 912
 QY 901 ACAGAGCAGTATGCTGCTGCGAGTTCTCTTACTTTTACCAGAGTGGTTGGATGT 960
 DB 913 ACAGAGCAGTATGCTGCTGCGAGTTCTCTTACTTTTACCAGAGTGGTTGGATGT 972
 QY 961 GAGTTAACTGGGTCATCAAAACCCCTTTTGTATACATCCATAGATGTTCTTGGTATTACA 1020
 DB 973 GAGTTAACTGGGTCATCAAAACCCCTTTTGTATACATCCATAGATGTTCTTGGTATTACA 1032
 QY 1021 AAG 1023
 DB 1033 AAG 1035

APPLICANT: HIGGS, Brandon
APPLICANT: CASTLE, Arthur
APPLICANT: ELASHOFF, Michael
TITLE OF INVENTION: Molecular Cardiototoxicology Modeling
FILE REFERENCE: 44921-5090-01-US
CURRENT APPLICATION NUMBER: US/10/338,044
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: US 60/303,819
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/305,623
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: US 60/377,611
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 2696
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2158
LENGTH: 3770
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. NM_022863
US-10-338-044-2158

Query Match 20.2%; Score 877.2; DB 6; Length 3770;
Best Local Similarity 91.6%; Pred. No. 3.7e-97;
Matches 940; Conservative 0; Mismatches 83; Indels 3; Gaps 1;

QY 1 ATGGACGCCCAAGACGAGTACGCCCTTTGAGTACCTTATTGAAACATTAATGACAGT 60
DB 12 ATGGACTCCCAAGTCAGGATACACCTTTGAGTACCTTATTGAAACATTAATGAGCAGT 71
QY 61 *TCACATAGAGTCTTCGATGTATCTAAACTT---GGCACCAGTATGATGTTCTGCCT 117
DB 72 TCACAGAAGAAGTCTTCAATGTACCTAAACTTGGAGGCCACCAAGTATGATTTCTGCCT 131
QY 118 TACTCAATACGGGCTTCTTGGAGAGTCTGTACGAAATGTGATGCTTTTAAATGAAG 177
DB 132 TACTCAATACGGGCTTCTTGGAGAGTCTGTACGAAATGTGATGATTTTAAATGAAG 191
QY 178 AAGGAAGATGTTAGACATTTTACGATGGAAGAACCAACCAAGCAATGTTGAAGTGCCC 237
DB 192 AAGGAAGATGTTATATAATATTTTGGACTGGAAGAACCAACCAAGCAATGTTGAAGTGCCC 251
QY 238 TTTTTCCTGCCCGTCTTCTTCAAGATTTTACTGGAATACCAAGCAATGTTGGATTTT 297
DB 252 TTTTTCCTGCCCGTCTTCTTCAAGATTTTACTGGAATACCAAGCAATGTTGGATTTT 311
QY 298 GCTGCTATGAGGAGGAGTGAAGCACTTCTGGAGTGATCTGAGAAAGTCCATCTCTGCT 357
DB 312 GCTGCTATGAGGAGGAGCAATGAAGCACTTCTGGAGTGATCTGAGAAAGTCCATCTGCT 371
QY 358 TGTCGACAGATCTTACAGTTGACCATCTTTACAAATTTGACTTACGATTAATGTCGAATA 417
DB 372 TGTCGACAGATCTTACAGTTGACCATCTTTACAGATTTGACTTACGATTAATGTCGAATA 431
QY 418 CAGATGACCAATCTCTGGAGTGGTGACCTGAGAAAGCAGGAAGCTCTCTCCACTT 477
DB 432 CAGATGACCAATCTCTGGAGTGGTGACCTGAGAAAGCAGGAAGCTCTCTCCACTT 491
QY 478 AAGTGCAGCCTAAGAGCTTCCCTGCGAGGCCAGACTACCTCCGAGGATCTGTGAT 537
DB 492 AAGTGCAGCCTAAGAGCTTCCATGTCGAGGCCAGACTACCTCCGAGGATCTGTGAT 551
QY 538 TCTGGAGAACTAGCCCGAAATCTAGGAACATTTTCTTCGCAATTTGAGATACACCCATC 597
DB 552 TCTGGAGAACTAGCCCGAAATCTAGGAACATTTTCTTCGCAATTTGAGATACACCCATC 611
QY 598 CTGTGCTCTTTTCAATTTGCAACAGCTGCTGAACTGAAACAGTGTAAAAATCAAGAA 657
DB 612 CTGTGCTCTTTTCAATTTGCAACAGCTGCTGAACTGAAACAGTGTAAAAATCAAGAA 671

QY 658 GTAGAAATTCGGCAGAAATCGAGAGGCTTCAGTTTTTTTAAAGTGGAGTTCAGAGTTTTTA 717
DB 672 GTAGAAATTCGGCAGAAATCGAGAGGCTTCAGTTTTTTTCAAGTGGAGCTCAGAGCTTTT 731
QY 718 AAGAATGTGGCAGTATCCCTCCTGGAACCTGGAATGGCTCATCAATAAATAACTTAGAATAT 777
DB 732 AAGAATGTGGCAGTATCCCTCCTGGAACCTGGAATGGCTCATCAAGTGAACATTAAGACAT 791
QY 778 TTGTCAGAGTGGTTTTTGAAGAAAGACCTCCTTCCAGACAGTGTATGTCGGCACA 837
DB 792 TTGTCAGAGTGGTTTTTGAAGAAAGACCTCCTTCCAGACAGCTGAATTTGGCACA 851
QY 838 GATTACACATAACGATGTTAGGATTTCTAGGATTTCTGGGTGGGGGTTGGAGGCATT 897
DB 852 GATTCTCATATAACCATGTTGGAATGATGGAATTTCTTGGGTGGGGAGTTGGAGCAT 911
QY 898 GAAACAGAAGCAGTATGCTTGGCTTGGCAGTTTCTCTTACTTTACCAGAGTGGTTGGA 957
DB 912 GAGACAGAGGCAGTTATGCTTGGCCTTGGCAGTTACTTACTTTACCAGAGTGGTTGGA 971
QY 958 TGTGAGTAACTGGGTCATCAAAACCTTTTGTACATCCATAGATGTTGTTCTTGGTATT 1017
DB 972 TGTGAGTAACTGGGTCATCAAACTGCTTTGTTACATCCATAGATATTGTTCTTAGGCATT 1031
QY 1018 ACAAG 1023
DB 1032 ACAAG 1037

RESULT 4
US-60-436-643-4106
; Sequence 4106, Application US/60436643
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Hepatotoxicology Modeling
; FILE REFERENCE: 44921-5038-P15
; CURRENT APPLICATION NUMBER: US/60/436,643
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/331,273
; PRIOR FILING DATE: 2001-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4295
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4106
; LENGTH: 3770
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. U20181
US-60-436-643-4106

Query Match									
Best Local Similarity 20.2%; Score 877.2; DB 7; Length 3770;									
Matches 940; Conservative 0; Mismatches 83; Indels 3; Gaps 1;									
Qy	1	ATGGAGCCCCAAAAGCAGGATACGCCCTTTGAGTACCTTATTGAAACATTAAATGACAGT	60						
Db	12	ATGGACTCCCAAGTGCAGGATACACCTTTGAGTACCTTATTGAAACATTAAATGGCAGT	71						
Qy	61	TCACATAGAAGTCTTCGATGTATCTAACTT---GGCACCAGTATGATGTTCTGCCT	117						
Db	72	TCACAGAAGAAGTCTTCAATGTACTTAACCTTTGGAGGCACCAAGTATGATTTCTGCCT	131						
Qy	118	TACTCAATACGGGTCTTCTTGGAGCTGCTGTACGAAATTCGTATGGCTTTTAAATGAAG	177						
Db	132	TACTCAATACGGGTCTTATTGGAAGCTGCTGTACGAAATTCGTATGATTTTAAATGAA	191						
Qy	178	AAGGAAGATGTTATGAACATTTTATAGCTGGAACCAACCAACAAAGCAATGTTGAAAGTCCC	237						
Db	192	AAGGAAGATGTTATAAATATTGGAAGTGGAAACCAACCAACAAAGCAATGTTGAAAGTCCC	251						
Qy	238	TTTTTCCCTGCCCGTCTTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTT	297						
Db	252	TTTTTCCCGCCCGTGTGTTCTTCAAGATTTTCACTGGAATACCGGCAATGGTGGATTTT	311						
Qy	298	GCTGCTATGAGGAGGCGAGTGAACACTCTTGGAGGTGATCCTGAGAAAGTCCATCCTGCT	357						
Db	312	GCTGCTATGAGGAGGCAATGAACACTCTTGGAGGTGATCCTAGAAAGTCCACCCCTGCC	371						
Qy	358	TGTCGACAGATCTTACAGTTGACATTTCTTTTACAAATTCAGTTCAGTAAATGCGCAATA	417						
Db	372	TGTCCACAGATCTCACAGTTGACACACTCTTTTACAGATTTGACTTCAGTAAATGTCGAATA	431						
Qy	418	CAGATGCACCAATCTGGAGGTGGTGACCTGCAGAAAGCAGGAAAGCTCTCCACTT	477						
Db	432	GAGAATGCACCAATCTGGAGGTGGTGACCTGCAGAAAGCAGGAAAGCTCTCCACTT	491						
Qy	478	AAAGTGCAGCCTTAAGAAGCTTCCCTGCGAGAGCCAGACTACTCTCCGAGGATCTTGAT	537						
Db	492	AAAGTACAGCCTTAAGAAGCTTCCATGTGCGAGCCAGACTACTCTCCGCGGATCGTGAT	551						
Qy	538	TCTGAGAACTAGGCCGAAACTCAGGAACATTTTCTTCGAGATGAGATACACCCATC	597						
Db	552	TCTGAGAACTAAGCCGAAACTCAGGAACATTTTCTTCGAGATGAGAAATACGCCCTGTC	611						
Qy	598	CTGTGCTCTTTTCAATTCGAACAGTGCCTGAACCTGAAACAGTGTAAATAACAAGAA	657						
Db	612	CTGTGCTCTTTTCAATTCGAACAGTGCCTGAACCTGAGACGGTGTAAATAACAAGAA	671						
Qy	658	GTAGAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTTAAAGTGGAGTTCGAAGTTTTA	717						
Db	672	GTAGAATTCGGCAGAAATCGAGAGAGGCTTCAATTTTTTCAAGTGGAGCTCAGGAGCTTT	731						
Qy	718	AAGAATGTGGCAGTATGCCCTCTCGGAATCGGAATGGCTATCAATAAATTAAGATAT	777						
Db	732	AAGAATGTGGCAGTATGCCCTCTCGGAATCGGAATGGCTATCAAGTGAACCTTAGAAT	791						
Qy	778	TTGTCAAGAGTGGTTTTGAAGAAAGACCTCTCTTCCAGACAGTGTAGTCGGCACA	837						
Db	792	TTGTCAAGAGTATGTTTTGAAGAGCCGACCTGCTCTTCCAGACAGCGTAAATTTGGCACA	851						
Qy	838	GATTCACACATTAACATGGTGAATGGTTTAGGGATTTCTGGGGTGGGGGTTTGGAGGCATT	897						
Db	852	GATTCATATAACCATGTTGAATGGATTGGGAATTTCTTGGGTGGGAGTTGGAGGCATT	911						
Qy	898	GAACAGAACAGATGATGCTGGCTGCCAGTTCTCTTACTTTACACAGAGTGGTGGGA	957						
Db	912	CAGACAGAGGAGTATGCTTGGCTGCCAGTTACTCTTACTTTTACCAGAGGTTGGTGA	971						
Qy	958	TGTGAGTTAACTGGGTGATCAAAACCTTTTGTACATCCATAGATGTTGTTCTTGGTATT	1017						
Db	972	TGTGAGCTAACTGGGTGATCCAAATGCTTTTGTACATCCATAGATATTTGTCCTAGGCATT	1031						
Query Match 15.1%; Score 654.8; DB 6; Length 5601;									
Best Local Similarity 77.1%; Pred. No. 1.1e-70;									
Matches 911; Conservative 0; Mismatches 112; Indels 159; Gaps 3;									
Qy	1	ATGGAGCCCCAAAAGCAGGATACGCCCTTTGAGTACCTTATTGAAACATTAAATGACAGT	60						
Db	95	ATGGACTCCCAAGTGCAGGATACACCTTTGAGTACCTTATTGAAACATTAAATGGCAAT	154						
Qy	61	TCACATAGAAGTCTTCGATGTATCTAAACTTGGCACCA-----	100						
Db	155	TCACAGAAGAAGTCTTCAATGTATCAACTTGGCGGCACCAAGTATGTGTAGACAT	214						
Qy	101	-----AGTATGATGTTCTGCTTACTCAATACGG	129						
Db	215	GACTTCTGTTTACGGTAATATTTTATCTTGAATCAGATATTTGCTTACTCAATACGG	274						
Qy	130	GTCTTGTGGAACTGCTGTACGAAATTTGTATGGCTTTTAAATGAAGGAAGATGTT	189						
Db	275	GTCTTATGGAAGTCTGCTGTACGAAATTTGTATGGCTTTTAAATGAAGGAAGATGTT	334						
Qy	190	ATGAACATTTTATGACGTGGAACCAACCAAGCAATTTGGAAGTGCCCTTTTCCCTGCC	249						
Db	335	ATGAACATTTTGTGACTTGGAAACCAACAGCAATGTTGAAGTGCCCTTTTCCCTGCC	394						
Qy	250	CGTGTCTTCTTCAAGATTTTACTGGAATACCAAGCAATGTTGATGTTTCTGCTATGAGG	309						
Db	395	CGTGTGTTCTTCAAGATTTTCACTGGAAATACCGGCAATGGTGGATTTTCTGCTATGAGG	454						
Qy	310	GAGGAGTGAACACTCTTGGAGGTGATCCTTGAGAAAGTCCATCCTTGTCCGACAGAT	369						
Db	455	GAGGAGTGAACACTCTTGGAGGTGATCCTTAAGAAAGTCCACCTGCTGTCGACAGAT	514						
Qy	370	CTTACAGTTGACCAATCTTTTACAAATTTGACTTCAGTAAATGTGCAATACAAATGACCA	429						
Db	515	CTCACAGTGGACACACTCTTTTACAGATTTGACTTCAGTAAATGTGCAATACAGAAATGACCA	574						
Qy	430	AATCTCGAGGTGGTGAACCTTGCAGAAAGCAGGAAAGCTCTCTCCACTTAAAGTGCAGCT	489						
Db	575	AATCTCGAGGTGGTGAACCTTGCAGAAAGCAGGAAAGCTCTCTCCACTTAAAGTGCAGCT	634						
Qy	490	AAGAAGCTTCCCTCGAGAGGCCAGACTTACCTGCGGAGGATCTTTGTGATTTCTGGAGACTA	549						
Db	635	AAGAAGCTTCCATGTCGAGGCCAGACTTACCTGCGGGGATCGTGTCTATCTTGGAGACTA	694						
Qy	550	GGCGAAACTCAGAACATTTTCTTCGCAGATTTGAGAAATACACCCATCTCTGTCTCTTT	609						
Db	695	AGCGGAACCTCAGGAACATTTTCTTACAGATTTGAGAAATACACCTGCTGTGTCTCTTT	754						
Qy	610	CATTTGCAACCTGCTGAACCTGAAACAGTCT-----TAAA	647						
Db	755	CATTTGCAACCTGCTGAGTATGACATTTGTTCTTGTAAATAGTTTTAGTCCAGTACT	814						

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QY 648 AAATCAAGAGTAGAATTCGGCAGAAATCGAGAGAGGGCTTCAGTCTTT----- 694
Db 815 TATTATAAATTGGAGTTGGTCAGATTGAGCAGTTGGCTAAACGTTTGTAGTGTCAATGTTT 874
QY 695 ----- 694
Db 875 ATTTGTATCTTGATTTATGAATACAGAGTTACACAGTGCACATTAATAACACTGTGTCTCTTC 934
QY 695 -----TTAAGTGGAGTTTCAAGAGTTTAAAGAGTTTGGCAGTGCATCCCTCCT 741
Db 935 AATCAACAATAACAGTGGAGCTCAGAGCTTTTAAAGATGTGGCAGTGCATCCCGCT 994
QY 742 GGAATCGGAATGGCTCATCAATAAATCAACTAGAAATATTTGCAAGAGTGGTTTTGAGAA 801
Db 995 GGAATCGGAATGGCTCATCAACTAGAAATATTTGCAAGAGTGGTTTTGAGAA 1054
QY 802 AAAGACCTCTCTTCCACAGAGTGTAGTCGCGCAGAGTTCCACATCAACGATGCTGAAT 861
Db 1055 ACGGACCTGTCTTCCACAGAGTGTAGTCGCGCAGAGTTCTCATATAACCATGCTGAAC 1114
QY 862 GCTTTAGGAGTCTCTGGGGTGGGGGTTGGAGGCATTGAAACAGAGCAAGTTATGCTTGGT 921
Db 1115 GGATGGGAGTCTTGGGTGGGAGTGTGGTGCATTGAGACAGAGGCAGTTATGCTTGGC 1174
QY 922 CTGCCAGTTTCTTCTTACCTTACCAGAGTGGTTGGATGTGAGTTAACTGGGTGCATCAAC 981
Db 1175 CTGCCAGTTTACTTCTTACTTTACAGAGTGGTTGGATGTGAGTTAACTGGGTGCATCAAT 1234
QY 982 CTTTGTGTACATCATAGATGTTCTTGGTATTACAAAG 1023
Db 1235 GCTTTTGTATCATCATAGATATTCTCTTGGCATTACAAAG 1276

RESULT 6.
US-09-949-004-699
; Sequence 699, Application US/09949004
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR GENES ASSOCIATED WITH DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000848
; CURRENT APPLICATION NUMBER: US/09/949,004
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/232,045
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 6961
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 699
; LENGTH: 47684
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(47684)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-004-699

Query Match 8.5%; Score 368; DB 5; Length 47684;
Best Local Similarity 61.8%; Pred. No. 9.3e-37;
Matches 697; Conservative 1; Mismatches 401; Indels 29; Gaps 6;

QY 2392 CATCTTAAAAATAAATCAATAGCGCGCGGCTGACGCTGTAAATCCAGCACT 2451
Db 38874 CAGACATAGTACACAAATATCGCGCGCGGCTGACGCTGTAAATCCAGCACT 38933
QY 2452 TTGGGAGCGCGAGCGGGTGGATCATGAGTTCAGGAGTCGAGACCATCTCGCTGAACAA 2511
Db 36934 TTGGGAGCGCGAGCGGGTGGATCATGAGTTCAGGAGTCGAGACCATCTCGCTGAACAA 38993
QY 2512 GGTGAACCCCGTCTCTACTATAAATACAAAAATATAGCCGGCGGGTGGCGGCGCT 2571
Db 38994 GGTGAACCCCGTCTCTACTATAAATACAAAAATATAGCCGGCGGGTGGCGGCGCT 39053
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QY 2572 GTAGTCCCAAGCTTCTCGGAGGCTGAGGCGAGGAGATGCGGTGAACCCCGGAGGCGGAGC 2631
Db 39054 GTAGTCCCAAGCTTCTCGGAGGCTGAGGCGAGGAGATGCGGTGAACCCCGGAGGCGGAGC 39113
QY 2632 TTGCAGTGCACCAAGATTGGCCACCTGCAGTCCGAGTCCGGCTCGGCGCAGACAGCGAG 2691
Db 39114 TTGCAGTGCACCAAGATTGGCCACCTGCAGTCCGAGTCCGGCGCAGACAGCGAG 39173
QY 2692 ACTCTGTCTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2745
Db 39174 ACTCTGTCTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 39233
QY 2746 TCTTTACACTTAGGTTTGGATTCTGTATCTATAAAGAGGTTTGGATTAGTGTATCC 2805
Db 39234 ATCACATATGGAAGCTAAAAAAGTGGTTATCGTGAATAAGAGTAGGTTCATGGTTAC 39293
QY 2806 CTGSCACTTATAAATCTTAGGGCTTAATATTATTCATAGATCGAGATAGTTTCTATTCT 2865
Db 39294 CAGAGGCTAGGAGGAGTGGGGAGGGGGCGAGAAAGAGA-----GGTGGATTCAAGGG 39348
QY 2866 TAGTCGCTCTCTTAGTCACCTCTTCCATATACCAATCTGAGACCACTTTTACAAATTTAGAAAA 2925
Db 39349 TACAAACATACAATTAATAGAGGACAAAGTTCTAGTGTCTAATAGCACAGTAGGGTGA 39408
QY 2926 GACAAATAACTGGTTGGTTACTGTATAGTATATAACCAAGAAAAATAATTTTAGAAG 2985
Db 39409 CTAGGCTTAACAACAGTTTTTATATATTTTCAAGAACTACCTAGAGAAAAAGATTTTGAATG- 39467
QY 2986 AATTAAGTTTGAACACACATGTTAACAAATCTACCAAAAGTGGATTTGCTCTGTATTA 3045
Db 39468 -----CTCCCAACACAAAGAAATGATTAATTTGTTGAAGTGTAGCTAGCTGATT--- 39518
QY 3046 AGATGCTGTAACATTTGGCCAGTAGTTATTAATTTGAAAAATGTTTATAGCAATATAT 3105
Db 39519 -GATCATTTACACATTTGATGCAATGATCAAAATATTCATTTGCCCCACAATATGTAAA 39577
QY 3106 AATTTTTTATTAATAATACAGTTTCACTAGCTATTAGTATTTCATTAAGTCTAAGTAG 3165
Db 39578 ATTATTATATGAAATTTTAAATCTTCAAGAAAAAATGTATATTATTCTAGAAATTC 39637
QY 3166 CCATCAGTGGTTAGCAACACCACCTGTTTTTATGCATGCTTAAGAAAGAAATAAAGGCTGT 3225
Db 39638 TAAGAAATACCTCTGTGGACCACCACTTTAAAAAAAACCTTAGGCCAGATGCTGTGGCTCAT 39697
QY 3226 GTGCAGTGGCTCACACCTGTGGGACGCCAAGGAGGAGCATCTTGAGGCGCAGAGTTTC 3285
Db 39698 GCTTGTATCCACACACTTTGGGAGGCTGAGTGGTGGATCACTTGGGGTTCAGGAGTTC 39757
QY 3286 AAGACCAACCTTGTCAACATTTGAAGACCTGCTCTACAAAAAATAAAGTTTAAAT 3345
Db 39758 GAGACCAGCTTGCCAAAATAGTGAACCCCATCCTATTAAAAATAC-----AAAAAT 39811
QY 3346 TAGCTGGGTGGGTGGCAGCATGCTGTAGTTCAGCTACTCTGGAGGCTAAGTGGGAGG 3405
Db 39812 TAGCCAGGTGTGATGGTGGGCGCTGTAATCCCACTACTCAGGAGTCTCAGGAGGAGAAA 39871
QY 3406 ATTCTAGAGCCACGGTGTGGAGCTGCAATGAGTGTGACACACACTGCGCTCCAG 3465
Db 39872 ATTCTTGAACCTGGGAGGAGAGGTTGCAATGAGCGAGATCATGCTCACTTCACTCCAG 39931
QY 3466 CGTGGGCAACAGTAGAGACCTCTTTTCTAAAGAAAAAGAAAAA 3513
Db 39932 CCT-GGTGACAGAGTGAGACTTTTCTCTTAAAGAAATAAATAAATAAATAA 39978

RESULT 7
PCT-US02-09734-3/c
; Sequence 3, Application PC/TUS0209734
; GENERAL INFORMATION:
; APPLICANT: PE CORPORATION (NY)
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
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;; TITLE OF INVENTION: AND USES THEREOF
;; FILE REFERENCE: CL001215PCT
;; CURRENT APPLICATION NUMBER: PCT/US02/09734
;; CURRENT FILING DATE: 2002-03-30
;; PRIOR APPLICATION NUMBER: 09/821,771
;; PRIOR FILING DATE: 2001-03-30
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 114693
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(114693)
;; OTHER INFORMATION: n = A,T,C or G
PCT-US02-09734-3

Query Match 8.2%; Score 356.6; DB 1; Length 114693;
Best Local Similarity 61.8%; Pred. No. 1.6e-35;
Matches 691; Conservative 1; Mismatches 355; Indels 72; Gaps 5;

QY 2401 AATAAAACCATAGGCGGCGGGTGGCTCAGCGCTGTAAATCCAGCACATTGGGAGGC 2460
DB 13329 AAAAAGAAAATAGCGCGGCGGGTGGCTCAGCGCTGTAAATCCAGCACATTGGGAGGC 13270

QY 2461 CGAGCGGGTGGATCATGAGGTGAGGATCGAGAGATCGAGACATCCTGGCTAAACAAGGTGAACCC 2520
DB 13269 CGAGCGGGTGGATCATGAGGTGAGGATCGAGAGATCGAGACATCCTGGCTAAACAAGGTGAACCC 13210

QY 2521 CCGTCTCTACTAAAATACAAAAATAGCCGGCGGGTGGGCGGCGCTGTAGTCCCA 2580
DB 13209 CCCTCTCTACTAAAATACAAAAATAGCCGGCGGGTGGGCGGCGCTGTAGTCCCA 13150

QY 2581 GCTTCTCGGAGGTGAGGAGGAGATGCGTGAACCGGGAGCGGAGCTTGCAGTGA 2640
DB 13149 GCTACTCGGAGGCTGAGGCGGAGATGCGTGAACCGGGAGCGGAGCTTGCAGTGA 13090

QY 2641 GCCAAGATTCGCCACTGTCAGTCCGCGCTCGGCGGAGAGAGAGCTCTGTGT 2700
DB 13089 GCCGAGATTCGCCACTGTCAGTCCGCGCTCGGCGGAGAGAGAGCTCTGTGT 13030

QY 2701 CAAAAAATAAAAAAATAAAAAAATAAATAGGAAACGAAGAATTAACCTTCAGTCACA --- 12973
DB 13029 CAAAAAATAAAAAAATAAAAAAATAAATAGGAAACGAAGAATTAACCTTCAGTCACA --- 12973

QY 2761 TTTGAGTTTCTGTATATAAAAAAGGGTTGGATTAAAGTGATCCCTGGCAGCTTATAAAA 2820
DB 12972 -----AAATATCAACATAAATAAAGA 12949

QY 2821 TGTTAGGGCTTAATATTATTCATGATGAGGATAGTTTTCATTTAGTCGCTCCTTAG 2880
DB 12948 TAATAGAGAGAAGTATTTATATAAGAAATATGAATTAATGAATAGAAAGAAATAA 12889

QY 2881 TCACCTTCTTACCAATCTGAGACCTTTTACAATTTAGAAAGACAAATAACTGGTT 2940
DB 12888 ACAAAAGAAATAACAA ---GAACAAAGCTGATCTTTTAAAAAATAAATAAGA 12833

QY 2941 GGGTTACTTGTATATAACCAAGAAATAATTTTAGAAGGAATTAAGTTTGAAC 3000
DB 12832 TAGCCCTCTGGTAGCTGATTAAGAAAGAAAGAAATATGAATATAGACTATTAGG 12773

QY 3001 CACATGTTAACAAATTTTACCAAGTGGGATTGGCTGTGATTAAGATGCTGTAAACAT 3060
DB 12772 AAAAAAATACATATACA -----GAGGAGATTAAGAAATAGAGGCCAGGCC 12721

QY 3061 TTGGGCCAGTAGTTAATTTGAATAATGTTTATAGCCAAATATATAATTTTATTATAA 3120
DB 12720 AGTGGCTAGCTGCTGAATCTCTGCACTTTGGGAGACCAAGGT----- 12678

QY 3121 TATACAGTTTCATCAGCTATTAGTATTTTCAATTAAGTCAAGATGCCATCAGCTGTAGC 3180
DB 12677 GAGAGGATCACTTGAGTCCAGGAGTTCAGACAGCAGCTGGGCAACATGGCAAAACCTGT 12618

QY 3181 AAACACCACTGTTTATGCACTGCTAAGAAAGAAATAAAGGCTGTGTGCAGTGGCTCACA 3240
DB 12617 CTCACAAAAAATACAAGGCTGGGTGGCGGGTGCAGTGGTTTACGCCCTATAATCCCAGC 12558

QY 3241 CCGTGGGAGCGCAAGGAGGAGCATCTTGGAGCCAGAGAGTTTCAAGACCAACCTGTGTC 3300
DB 12557 ACTTTGGGACACCAAGTGGGAGGATTGCTTAAGCCAGAGAGTTCAAGACCAACCTGGGT 12498

QY 3301 AACATTGTAAGACCCCTGCTCTACAAAAAATAAAGTAAAAATAGCTGGTGGCGGTG 3360
DB 12497 AACATGTCAAAACTTTGTCTCTACAAAAATAAT----TAAAAATTAGCTGAGCATAGTG 12442

QY 3361 GCACATGCTGTAGTTCAGGCTACTCTGGAGGCTAAGCTGGGAGGATTGCTAGAGCCACG 3420
DB 12441 GTGCACGCTGTAGTCTCACCTACTTTGGAGGCTGAGTGGGAGGATCACTGGAGCCAG 12382

QY 3421 GTGTGGAGCTGCAATGAGCTGTGACCAACACCACTCGCTCCAGCTGGGCAACAGAGT 3480
DB 12381 GAGTGCCAGGCTGCAGTGTGATGGCTGCTGCTCCACCTTAGCAACAGAGT 12322

QY 3481 GAGACCCCTGTTCTAAAGAAAGAAAGAAAGGCGTG 3519
DB 12321 GAGACCCCTGTTCTCAAAAAAATAAAGAAAGAAATGAATG 12283

RESULT 8
US-10-301-844-1/G
; Sequence 1, Application US/10301844
; GENERAL INFORMATION:
; APPLICANT: Ruddy, David A.
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
; HEMOCHROMATOSIS GENE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/301,844
; FILING DATE: 20-Nov-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,495C
; FILING DATE: 07-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0057-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-301-844-1

Query Match 7.7%; Score 336.4; DB 6; Length 235033;
Best Local Similarity 59.8%; Pred. No. 3.4e-33;

Matches	580;	Conservative	1;	Mismatches	432;	Indels	25;	Gaps	6;
QY	2386	TTCTTTTCATCTAAAAATAAAACCATAGCGCGCGCGGTGGCTACGCGCTGAATACCC	2445						
Db	132389	TTATATTTCCTTGGATAAAGTCAGTAGGCGGCGCGGTGGCTATGCGCTGTCATCT	132330						
QY	2446	AGCACTTTGGGAGCGCGGAGGGGTGGATCATGAGGTGAGGATCGAGACCATCTGGC	2505						
Db	132329	AGCACTTTGGGAGGTGAGTGGGAGATCATGAGTCTAGGATCGAGACCATCCCGCG	132270						
QY	2506	TAAACAAGGTGAACCCCGCTCTACTATAAATACAAAAATATAGCCGGCGGTGGCGG	2565						
Db	132289	TAAACGGTGAACCCCTGCTCTACTAAAAATACAAAAATATAGCTGGCGGTGGCGG	132210						
QY	2566	CGCGCTAGTAGCCCAAGCTTCTCGGAGGCTGAGGCAGGAGATGCGGTGAACCGGGAGG	2625						
Db	132209	CGCGCTGTGGTCCAGCTACTCGGAGGTTGAGGCAGGAGATGCGGTGAATCCGGGAGG	132150						
QY	2626	CGGAGCTTGCAGTGAGCCAAAGATGCGCCACTGCGAGTCCGCGAGTCCGCGTGGCGACAG	2685						
Db	132149	CGGAGTGTGCAGTGAGCGCGAGATTGTGCCACT-----GCATTCCAGCTGGCGGACAG	132097						
QY	2686	AGCGAGACTCTCTTCACAAAAAATAAAAAAATAAAAAAATAAAATGAGGAACGCA	2745						
Db	132096	AGCAAGACTCCGCTTCACAAAAAATAAAAAAATAAAAAAATAAAATGAGGAATAA	132037						
QY	2746	TCCTTTACACTTAGGGTTTGAGTTCTGTATCTATAAAAAAGGTTTGATTAAGTGATCC	2805						
Db	132036	TGCATTTCCTTTGGGACTTTTAATATTAGTCTACAAATCTAGCCACCATAGAATCTGC	131977						
QY	2806	CTGGCACTTAATAATGTTAGGGCTTAATATTATCATAGATCGAGGATAGTTCATTCT	2865						
Db	131976	TGATTAATAACGGGTTCTGTTAAAAATGAAACATGCAATTTTGGGGAAAAAGAGGAGT	131917						
QY	2866	TAGTCGCCCTCTTAGTCACTCTTCCATACCAATCTGAGACCATTTTACAATTTAGAAAA	2925						
Db	131916	GTTTTAGTGATTTTGTGTTTTTACACTGTTTATAATAAAATTTTAAGCAATCTTGAGGGG	131857						
QY	2926	GACAAATAACCTGGTTGGGTTACTGATAGTATAATAACCAAGAAAAATAATTTAGAGG	2985						
Db	131856	AACATTTTATTTCTACTGTGAAGTGCATAAAGTTATGAGATTAAGTTACAAGCTATATCA	131797						
QY	2986	AATTAAGTTTGAACACCATG--TTACAATAATCTACCAAGTGG-GATTTGCCCTGTGAT	3042						
Db	131796	CATACAGTTTGTAGCTTTATAAATTTAGAAATCTTAACAGAATAAATATGCTAATATGAT	131737						
QY	3043	TAAAGATGCTGAACATTTGGCGCCAGTGTATAATTGAAAAATGTTTATAGCCATA	3102						
Db	131736	GAAATGTCATAAATTCATTTAGATATATTTTATAAACCAATTCAGAAGGACCAATA	131677						
QY	3103	TATAATTTTTTATTAATAATACAGTTTCATCAGTCTA-----TTAGTATTTCATTAA	3155						
Db	131676	CCCAATTTCAAAATCATATTAAATTGTAAATTAATAGGGCAGCCAAAATATTCTGGAT	131617						
QY	3156	GTCTAAGATGCCATCAGTGGTTAGCAACACCATGTTTTATGCACTGCTAAGAAAAAAT	3215						
Db	131616	TCCTTCTAATAAACAATAAGTGTAAATACAGTCTGACTGACAAATCTGAAGAATATG	131557						
QY	3216	AAAGGCTGTGTGAGTGGCTCACACCTGTGGGACGCCAAGGCAGGAGCATCACTTGAGG	3275						
Db	131556	CAGCATAAAGTGATTATCCCGACCTTTGGGAGGCGAAGGTGGGAGATCA--TGAGG	131499						
QY	3276	CCAGAAGTTCGAAGACCAACCTGGTCAACATGTGAAGACCTGTCTCTACAAAAAATAA	3335						
Db	131498	TCAGAGTTGGAGACCAAGCCTGACCAACATGGTGAACCCCGCTTTTACTAAAAATA---	131442						
QY	3336	AGTTAAAAATTTAGCTGGGTGGGTGGGCACATGCTGTAGTTTCCAGCTACTCTGAGGCTA	3395						
Db	131441	---CAAAAAATAGCCGGGCTTGGTGGTGCACACCTGTAATCCAGCTGCTCAGGAGGCTA	131385						
QY	3396	AGGTGGGAGGATTCCTAGAGCCACCGTTGTGGAGCTGCAATGAGCTGTGACCAACAC	3455						
Db	131384	AGGCAGAGAACTCCTTGAATCCAGAGAGTGTGAAGTTGCAATGAAGCAAGATCAGGCAC	131325						

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QY 3456 TGCCTCCAGCGTGGGCAACAGAGTGAGACCTGTTTCTTAAAGAAAGAAAGAAAA 3513
||| ||||| ||||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 131924 TGCACCTCAGCCTGGGCGAGAGAGTGACTCTGACTCAAAAAAATAAATAAATA 131267

RESULT 9
US-10-301-844-2/c
; Sequence 2, Application US/10301844
; GENERAL INFORMATION:
; APPLICANT: Ruddy, David A.
; Wolff, Roger K.
; TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
; HEMOCHROMATOSIS GENE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/301,844
; FILING DATE: 20-Nov-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,495C
; FILING DATE: 07-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0057-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237326 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-301-844-2

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	Query Match	7.7%; Best Local Similarity Matches 680;	Score 336.4; Pred. No. 3.4e-33; Conservative 1;	Mismatches 432; Indels 25; Gaps	Length 237326;
QY	2386	TTCTTTCATCCTAAAAAATAAAACCATAGGCGGGCGGTGGCTCACGCCGTATATCCC	2445		
Db	134565	TTATATTCTTTTGATPAAGTCAAGTAGGCGGGCGGTGGCTCATGCCTGTGATCT	134506		
QY	2446	AGCACTTTGGAGCGCCGAGCGGGTGGATCATGAGTTCAGAGATCGAGACCATCTCGC	2505		
Db	134505	AGCACTTTGGAGGCTTGAGTGGGCAGATCATGAGTTCAGGAGATCGAGACCATCCCGC	134446		
QY	2506	TACAAGGTGAACCCCGTCTCTACTAAAAATACAAAATATTAGCGGGCGGTGGCGG	2565		
Db	134445	TACACGGTGAACCCCTGTCTCTACTAAAAATACAAAATATTAGCTGGCGGTGGCGG	134386		
QY	2566	GCGCCTCTAGTCCAGCTTCTCGGGAGCGTTCAGGCGAGGAATGGCTGAACCCGGGAG	2625		
Db	134385	GCGCCTGTGTCCAGCTACTCGGAGGTTTCAGGCGAGGAATGGCGTGAATCCGGGAGG	134326		
QY	2626	CGGAGCTTGCAAGTGAGCCAAGATTGGCCCACTCGAGTCCCGCTCGGCGACAG	2685		

D	b	134325	CGGAGGTTCGACGTAGCCGGAGATTGTGCCACT-----GCATTCACGCTGGGGCAGAC	134273
Q	y	2686	AGCGAGACTCTGYTTCANAAAAAAGAAAAAAAAAAACCATATAATAGAGAACAACGA	2745
D	b	134272	AGCAAGACTCCGTCAGAAAAGAAAAAAGTCACTAAAAATTAAGAGAAAAA	134213
Q	y	2746	TCITTACACTTAGGGTTTGAGTTTCGTATCTATAAAAAGGGTTTGGATTAAGTGAATCC	2805
D	b	134212	TGCATTTGCTTTGGGACATTTTAATATTTAGTCTACAANAATCTAGCCACCATAGAAATCTGC	134153
Q	y	2806	CTGSCACTTTAAAAATGTTAGGGCTTTAAATATTATTCATAGATCGAGGATAGTTTTCATTCT	2865
D	b	134152	TGATTAATACGGGTCTCTGTTAAATGGAACATGCATTTTGGGGAAAAAGAGGGACT	134093
Q	y	2866	TAGTCGCTCCTTAGTACACTCTCCCTATACCAATCTGAGACCATTTTACAATTTAGAAAA	2925
D	b	134092	GTTTTAGTGATTTTGTTTTTCACCTTGTTTATAATAAAAAATTTAAGCAATCTTGAGGG	134033
Q	y	2926	GACAAATACTGCTTGGGTACTTGATATAATAACCAAGAAAAATAATTTTACAAGG	2985
D	b	134032	AACATTTATTCTACTGTGTAACATGCAATAAGTTATGAGATAAAGTTACAAGCTATATCA	133973
Q	y	2986	AATTAAGTTTGAACACCACATG--TTAACAAATCTTACCAAAGTGG-GATTTGCCTGTGAT	3042
D	b	133972	CATACACTTTGTAGCTTTATAAATTTAGAAATCTTAACAGATAAATATGCTAAATATGAT	133913
Q	y	3043	TAAAGATGCTGTAAACATTTGGGCCAGTAGTTATAATTTGAAANAATGTTTATAGCCAATA	3102
D	b	133912	GAAATGCTATAAATTACATPAGAATATATTTTAATAAACCAATTCAGAAGGAGGCCAATA	133853
Q	y	3103	TATAATTTTTTATTAAATATACAGTTTTCATCAGTCTA-----TTACTATTTTCATTAA	3155
D	b	133852	CCCANTTTCAAAATCATATTAAITGTAAAAATTAANTTAGGCAGCCNAATATTCGGAAAT	133793
Q	y	3156	GTCTPAGATGCCATCAGTGGTTTAGCAAAACACCACACTGTTTTTATGCACTGCTAAGAAAGAT	3215
D	b	133792	TCITTCTTAATAAACAANAATGAGTGTAAATACAGTCGTACTGCAAAATCTGAGAAATATG	133733
Q	y	3216	AAAGGGCTGTGTCAGTGGCTCACACTGTGGGACCCCAGGCAGAGCATCACTTTGAGG	3275
D	b	133732	CAGCATAAAAGTGATATCCCCAGCACTTTGGGAGCCCAAGGTGGGCAGATCA--TGAG	133675
Q	y	3276	CCAGAAGTTCAAGACCACCACTGGTCAACATTTGTAAGACCTGTCTCTACAAAAAAGAAAA	3335
D	b	133674	TCAGGAGTTGGAGACCAGCCTGACCAACAATGGTGA AACCCGCTCTTTACTAAAAATA---	133618
Q	y	3336	AGTTAAAAATTAGCTGGGTGGGTGGGCATNGCCTGTAGTTCACAGCTACTCTGGAGGCTA	3395
D	b	133617	----CAAAAAATTAGCCGGGCTTGGTGGTGGCACACTCTTAATCCCAAGCTGCTCAGGAGGCTA	133561
Q	y	3396	AGGTGGGAGGATTGCTAGAGCCACGGTGTGTGAAGCTGCAANTGAGCTGTGACACACCAAC	3455
D	b	133560	AGGCAGGAGAACTGCTTGAATCCAGGAGGTGGAAGTTGCAGTAAGCCAGATCAGCCAC	133501
Q	y	3456	TGCGCTCCAGCGTGGGCCAACAGAGTGAGACCCCTGTTTCTTAAAAAGAAAGAAAAA	3513
D	b	133500	TGCATCCAGCTCGGGGCACAGAGTGTGACTCTGACTCAAAAAAATAAATAAATAAATA	133443

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RESULT 10
US-09-948-124-7/c
; Sequence 7, Application US/09948124
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON CHROMOSOME 7, HUMAN GENOME, AND USES THEREOF
; TITLE OF INVENTION: Y, METHODS OF DETECTION, AND USES THEREOF
; FILE REFERENCE: CL001301
; CURRENT APPLICATION NUMBER: US/09/948,124
; CURRENT FILING DATE: 2002-12-23
; NUMBER OF SEQ ID NOS: 183
; SEQ ID NO 7
; LENGTH: 4384464
; TYPE: DNA

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; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(438464)
; OTHER INFORMATION: n = A,T,C or G
US-09-948-124-7

Query Match          7.5%; Score 325.8; DB 5; Length 438464;
Best Local Similarity 58.4%; Pred. No. 2.6e-32;
Matches 668; Conservative 1; Mismatches 42; Indels 46; Gaps 4;

QY 2412 TAGGCGGCGCGGTGGCTCAGGCTGTAAATCCAGCACATTTGGGAGGCGGAGGGGTG 2471
    |||||
Db 957133 TGGGCGGCGCGGTGGTTCACGCTGTAAATCCAGCACATTTGGGAGGCGGAGGGTGGG 957074
    |||||

QY 2472 GATCATGAGTTCAGGAGATCGAGACATCTCGGTCTAAAGGTGAACACCCGCTCTACT 2531
    |||||
Db 957073 GATCAGAGGTTCAGGAGATCGAGACATCTCGGTCTAAAGGTGAACACCCGCTCTACT 957014
    |||||

QY 2532 AAAATACAAAAATTAGCGGCGCGGTGGCGGCGGCTGTAGTCCAGCTTCTCGGA 2591
    |||||
Db 957013 AAAATACAAAAATTAGCTGGCGGTGGCGGCGGCTGTAGTCCAGCTTCTCGGA 956954
    |||||

QY 2592 GGTGAGGACAGAGATGGCGTGAACCGGAGCGGAGCTTGCAGTGAGCCAAATTCG 2651
    |||||
Db 956953 GGTGAGGACAGAGATGGCGTGAACCGGAGCGGAGCTTGCAGTGAGCCAAATTCG 956894
    |||||

QY 2652 GCCACTTCGAGTCCGCGAGTCCGCGCTGGCGACACAGCGGAGACTCTGTTCAAAAAAAA 2711
    |||||
Db 956894 GCCACTTCGAGTCCGCGAGTCCGCGCTGGCGACACAGCGGAGACTCTGTTCAAAAAAAA 956841
    |||||

QY 2712 AAAAAA-----AAAAAACCATTAAT 2734
    |||||
Db 956841 AAAAAAAGCTTTTGTGTTTATCCACCAAAATTTGTATACCAACATTTATTTATAT 956781
    |||||

QY 2735 GAGGAACGCATCTTTACACTTAGGTTTGATTTCTGTATCTATAAAAGGGTTTGA 2794
    |||||
Db 956780 GCATATAGATGATTTAAATTTAATTAACCAAGTCAGTATTACTATACAAAGTGTGATG 956721
    |||||

QY 2795 TTAAGTGATCCCTGGCAGCTTATAAATCTTAGGCTTAATATTATTCATAGATCGAGGAT 2854
    |||||
Db 956720 TCTGTGTTTGTCTTTCACATTAAGTATGCTTGCAGAAATTTCTACATTAAGAAGATAG 956661
    |||||

QY 2855 AGTTTCATTTAGTCGCCTCTAGTCACCTCTTCCATACCAATCTGAGACCATTTTAC 2914
    |||||
Db 956660 ATATATCTCATTTATTTAGCGGTGCGATGGTATTCTAATGACTTTGATGCAACCATGACTG 956601
    |||||

QY 2915 AATTTAGAAAAGACAAATAACTGGTTGGGTACTGTGATGATATATAACCAAGAAATA 2974
    |||||
Db 956600 ATTAACTCTGTCATAACTATTTAGGTAATGCTAGATTTTAGCTAAACAGACAAATGCT 956541
    |||||

QY 2975 ATTTTAGAGGAATTAAGTTTGAACACCATGTTAAACAAATCTTACCAAGTGGGATTTG 3034
    |||||
Db 956540 GCAATGAATATCATTTGAGCAGAAATTTGAATGCTCTATTACTAGCTATCTGTCTGGA 956481
    |||||

QY 3035 CCTGTGATTAAGATGCTCTAAACATTTTGGGCCAGTAGTTATATTTGAAAAATGTTTAT 3094
    |||||
Db 956480 ACAATGGAATTTGTGATGAAGAAGATGCGAAGTTTATTTATAAAATTTTCAATCAT 956421
    |||||

QY 3095 AGCCAATATATATTTTATTTAAATATACAGTTTTCATCAGCTATTAGTATTTTCATTTA 3154
    |||||
Db 956420 TAAGAAAAAGACTGATAATACATTAATTTTCTCTATCTCTTAATTTTCAAGATTAACC 956361
    |||||

QY 3155 AGTCTAAGATG-CCATCAGTGGTTAGCAACACCACTGTTTATGCACTCTTAAGAAAGA 3213
    |||||
Db 956360 ATTTCGCCATGATGTGTGCATATCACCTTTTATTTAAANNTTGAACCTCTTGGCTGGGC 956301
    |||||

QY 3214 ATAAAGGGCTGTGTGCAGTGGCTCACACCTGTGGGAGCCCAAGGACGAGCATCTCTTGA 3273
    |||||
Db 956300 ACAGTGGCTCACGCCCTGTAAATCCAGCACTTTGGGAGGCTGAGCGAGTGGATCACTGA 956241
    |||||

QY 3274 GGCCAGAAGTTCGAAGCAACCACTGGTCAACATTTGAAGACCTCTCTCTACAAAAAAA 3333
    |||||

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Db	956240	GGTCAGAGCTTC	AAGACCATCTTTGGCCACATCGGTGA - AACCGGTCTACAAAAA	956182
Qy	3334	AAAGTTAAAAATTAGCTGGGTGGGTGGCACA	TGCCTGTAGTTCCAGCTACTCTGGAGC	3393
Db	956181	AAGAAAAAATCAGCAGGACGTGGCAGTGGG	ACCTGTAAATCCAGCTACTTTGGCAGC	956122
Qy	3394	TAAGGTGGGAGGATTGCTAGACCCACGGTGT	TTGGAAGCTGCAATAGCTGTGACCACACC	3453
Db	956121	TGAGGC	AAAGAAATTCCTTGAATCCGGAGCAGAGTTGCAGTAAAGCAGATCGCGC	956062
Qy	3454	ACTCGCTCCACGCGTGGGCAACAGATGAGAC	CCCTCTTTCTAAAGAAAGAAAGAAAAA	3513
Db	956061	ACTGCATCCAGCCTGGGCACAGAGTGAATTC	CAATCTCATATAAAAAA	956002
Qy	3514	GGG	3516	
Db	956001	AGG	955999	

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RESULT 11
PCT-US02-25201A-1/c
; Sequence 1, Application PC/TUS0225201A
; GENERAL INFORMATION:
; APPLICANT: APPLERA CORPORATION et al.
; TITLE OF INVENTION: Estrogen Receptor Alpha Variants And
; TITLE OF INVENTION: Methods Of Detection Thereof
; FILE REFERENCE: CL000258PCT
; CURRENT APPLICATION NUMBER: PCT/US02/25201A
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/933,267
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 465237
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-25201A-1

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Query Match	7.3%	Score 317.4;	DB 1;	Length 465237;
Best Local Similarity	93.5%;	Prod. No. 5.1e-31;		
Matches 330;	Conservative 1;	Mismatches 22;	Indels 0;	Gaps 0;
QY 2387	TCCTTTCATCCCTAAAAAATAAACCATAGGCGCGCGGTGCAGCTCTGAATCCCA	2446		
Db 47735	TATTTTCCCTTAGGCACAGAGCGCCAGTGGCGCGCGGTGCAGCTCTGAATCCCA	47676		
QY 2447	GCACCTTTGGAGGCGCGAGCGGGTGGATCATGAGGTCAGGAGATCCAGACCATCTCTGGCT	2506		
Db 47675	GCACCTTTGGAGGCGCGAGCGGGTGGATCATGAGGTCAGGAGATCCAGACCATCTCTGGCT	47616		
QY 2507	ACAAAGGTGAACCCCGTCTCTACTAAAAATACAAAAATTAGCCGGCGCGTGGCGGG	2566		
Db 47615	ACAAAGGTGAACCCCGTCTCTACTAAAAATACAAAAATTAGCCGGCGCGTGGCGGG	47556		
QY 2567	CGCCTGTAGTCCCGAGCTTCTCGGAGAGCTGAGCGCAGGAGATGGCGTGAACCCGGGAGGC	2626		
Db 47555	CGCCTGTAGTCCCGAGCTTCTCGGAGAGCTGAGCGCAGGAGATGGCGTGAACCCGGGAGGC	47496		
QY 2627	GGAGCTTGAGTGAGCCCAAGATTCGCGCACTGCCAGTCCCGAGTCCCGCGCTGGCGGCACAGA	2686		
Db 47495	GGAGCTTGAGTGAGCCCGAGATTCGCGCACTGCCAGTCCCGAGTCCCGCGCTGGCGGCACAGA	47436		
QY 2687	GGGAGACATCTGTGTCAAAAAAATAAAAAAATAAAAAAATAAAATGAGGA	2739		
Db 47435	GGGAGACATCTGTGTCAAAAAAATAAAAAAATAAAAAAATAAAATGAGGA	47383		

RESULT 12
US-60-427-045-313/c
; Sequence 313, Application US/60427045
; GENERAL INFORMATION:
; APPLICANT: The Board of Trustees of the University of Arkansas

```

: APPLICANT: O'Brien, Timothy
: APPLICANT: Beard, John
: APPLICANT: Underwood, Lowell
: TITLE OF INVENTION: Cal25 Gene and its Use for Diagnostic and Therapeutic
: TITLE OF INVENTION: Interventions
: FILE REFERENCE: 022438.44514
: CURRENT APPLICATION NUMBER: US/60/427,045
: CURRENT FILING DATE: 2002-11-15
: NUMBER OF SEQ ID NOS: 314
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 313
: LENGTH: 14277
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(66)
: OTHER INFORMATION: Exon C1
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1802)..(1947)
: OTHER INFORMATION: Exon C2
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (4198)..(4350)
: OTHER INFORMATION: Exon C3
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (4679)..(4747)
: OTHER INFORMATION: Exon C4
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (6811)..(6978)
: OTHER INFORMATION: Exon C5
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (11232)..(11270)
: OTHER INFORMATION: Exon C6
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (11594)..(11677)
: OTHER INFORMATION: Exon C7
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (13375)..(13500)
: OTHER INFORMATION: n is a, c, g, or t
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (14095)..(14187)
: OTHER INFORMATION: Exon C8
:
: US-60-427-045-313
:
: Query Match 7.3%; Score 315.6; DB 7; Length 14277;
: Best Local Similarity 59.7%; Pred. No. 2.4e-30;
: Matches 668; Conservative 1; Mismatches 415; Indels 34; Gaps 7;
:
QY 2400 AAATAAACCATTAGGCGGGCGGCTCAGCGCTGTAATCCACGACTTTGGGAGG 2459
Db 8758 AAAAAAAATTTGGGGCTGGGTGTGGTCTACGGCTGTAATCCACGACTTTGGGAGG 8699
QY 2460 CCGAGGCGGTTGGATCATGAGGTCAGGAGATCGAGACCATCTTGGCTTAACAGGTGAAC 2519
Db 8698 CCCAGTTGGCAGATCACGAGGTGAGAGATCGAGACCATCTTGGTCAACATGTTGAAC 8639
QY 2520 CCCGCTCTCTACTAAAAATAC--AAAAAATTAGCGGGCGCGGTGGCGGGCGCCTGTAGTC 2577
Db 8638 CCTGTTTCTCTAAAAATACAAAAAATTAGCCAGACATGTTGGCAGGCGCCTGTAGTC 8579
QY 2578 CCAGCTTCTCGGAGGCTGAGGCGAGAGATGCGGTCAACCCCGGAGGCGGACTTGCAG 2637
Db 8578 CCAGCTACTCAGGAGGCTGAGGAGGAAATGGCATGAACCCAGGAGGCGGACTTGCAG 8519
QY 2638 TGAGCCAAAGATTGGCGGCACCTGCAGTCCGCGCTTGGGCGACAGAGCGAGACTCTG 2697

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QY 2461 CGAGCGGTGATCATGAGTCAAGATCGAGACCATCTGGCTAAACAAGGTGAAC 2520
|||||
Db 258189 CGAGCGGTGGATCATGAGTCAAGATCGAGACCATCTGGCTAAACAAGGTGAAC 258248
|||||
QY 2521 CCGTCTCTACTATAAAATACAAAAATAGCGGCGCGGTGGCGGCGCCCTGTAGTCCCA 2580
|||||
Db 258249 CCGTCTCTACTATAAAATACAAAAATAGCGGCGCGGTGGCGGCGCCCTGTAGTCCCA 258308
|||||
QY 2581 GCTTCTCGGAGGCTGAGGAGGAGATGGCGTGAACCCCGGAGCGGAGCTTGCACTGA 2640
|||||
Db 258309 GCTACTCGGAGGCTGAGGAGGAGATGGCGTGAACCCCGGAGCGGAGCTTGCACTGA 258368
|||||
QY 2641 GCCAAGATTGGCCACTCGACTCGCGCTCGCGCTGGCGGACAGAGACACTCTCT 2700
|||||
Db 258369 GCCGAGATTGGCCACTCGACTCGCGCTCGCGCTGGCGGACAGAGACACTCTCT 258428
|||||
QY 2701 CAAAAAATAAAAAAAAAAAAAACCATAAATGAGGAACG 2743
|||||
Db 258429 CAAAAAATAAAAAAAAAAAAAAGCAGGAAGG 258471
|||||

RESULT 15
US-09-948-124-60/c
; Sequence 60, Application US/09948124
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON CH
; FILE OF INVENTION: Y, METHODS OF DETECTION, AND USES THEREOF
; FILE REFERENCE: CLO01301
; CURRENT APPLICATION NUMBER: US/09/948.124
; CURRENT FILING DATE: 2002-12-23
; NUMBER OF SEQ ID NOS: 183
; SEQ ID*NO 60
; LENGTH: 859705
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(859705)
; OTHER INFORMATION: n - A,T,C or G
US-09-948-124-60

Query Match 7.2%; Score 312.6; DB 5; Length 859705;
Best Local Similarity 61.8%; Pred. No. 1.6e-30;
Matches 705; Conservative 1; Mismatches 397; Indels 37; Gaps 10;
QY 2392 CATCTTAAAAATAAAACCATAGCGGCGCGGTGCTCAGCGCTGTAATCCCGCACT 2451
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Db 584148 CACCGATAAAATAGCAATGCGCGCGCGGTGCTCAGCGCTGTAATCCCGCACT 584089
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QY 2452 TTGGGAGCGCGAGGCGGTGATCATAGGTCAGGAGATCGAGACCATCTGGCTAACAA 2511
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Db 584088 TTGGGAGCGCGAGGCGCGGATCAGAGGTGAGGAGATCGAGACCATCTGGCTAACAA 584029
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QY 2512 GTGTAACCCCGCTCTCTACTATAAAATACAAAAATAGCGGCGCGGTGCGGCGGCT 2571
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QY 2572 GTAGTCCCAAGCTTCTCGGAGGCTGAGGAGGAGATGCGGTGAACCCGGAGCGGAGC 2631
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QY 2632 TTGCAGTGAGCAAGATTGCGGCATGCGAGTCCGCGCTCGCGCTGGCGGACAGCGAG 2691
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Db 583795 AGTGCTGGTGGTAATAACTTGTCTAGCCACACAGAGAAATGAA--ACTGGATCCTTAAC 583738
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QY 2932 TAACTGGTTGGGTACTTGTATAGTATAATAACCAAGAAAAATAAT--TTTAGAAGAAAT 2989
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QY 2990 AACTTTGAAACACACATGTTTAAACAAATCTTACCAAACTGGGATTTGCTGTGATTAAGAT 3049
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QY 3050 GCTGTAAACATTTGGGCCAGTAGTTATAATTTGAAAAATGTTTATAGCAATATATAATT 3109
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QY 3110 TTTTATTAAATATACAGTTTCATCAGTCTATTAGTATTTCATTAA-GTCTAAGATGCCA 3168
Db 583441 TCCAGAAATCTACAAAGAACTTAAACAAATCAACAAACAAAAACAAATGACCGCACTAAA 583382
QY 3169 TCAGTGGTTAGCAACACACACTGTTTATGCACTGCTAAGA-AAGAATAAAGGGCTGTGT 3227
Db 583381 AATGGACAAGGTTATGAAAGGTTATGCTACTAAAAGAGGACATTTACAGGGCGCGGC 583322
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Search completed: February 28, 2003, 14:54:38
Job time : 21575 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run On: February 28, 2003, 00:23:22 ; Search time 5553 Seconds
(without alignments)
12666.486 Million cell updates/sec

Title: US-09-730-559B-7
Perfect score: 4343
Sequence: 1 atgacgcgccccaaagcagg.....attcacagcagtcctctct 4343

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_htc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
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16: em_estom: *
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24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rod: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	717.4	16.5	954	14	BM802385
3	648.6	14.9	1068	12	BG260015
4	626.8	14.4	938	12	BG387889
5	616.6	14.2	1076	14	BQ224816
6	578	13.3	664	10	AV759698

7	510	11.7	754	12	BF669398
c	8	494.2	581	14	N63786
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	10	485.6	567	9	AA104450
	11	482.8	498	9	AA313478
	12	463.8	467	9	AL121430
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c	31	308.6	669	17	AQ108614
	32	308.4	549	17	B55844
	33	308	661	17	AQ415932
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ALIGNMENTS

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ACCESSION BQ433500
VERSION BQ433500.1
KEYWORDS GI:21172576
SOURCE EST.
ORGANISM human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 875)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM3208
row: j
column: 11
High quality sequence stop: 652.
Location/Qualifiers
1. .875

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AA104450 mo45a10.r
AA313478 EST185363
AL121430 DKFp7621
BF575050 602134712
BG258171 602379272
N94143 za25a11.f1
BQ333861 CM2-MT010
BE376722 601226569
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AV761302 AV761302
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AJ455338 AJ455338
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BI494159 df108b04.
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BQ025061 UI-1-BB1p
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/lab_host="DH10B (phage-resistant)"
/site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
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Note: this is a NIH_MGC Library."

BASE COUNT      251 a  185 c  197 g   242 t
ORIGIN

Query Match      18.3%; Score 794.6; DB 14; Length 875;
Best Local Similarity 99.2%; Pred. No. 7.8e-89;
Matches 820; Conservative 0; Mismatches 4; Indels 3; Gaps 2;

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QY  121  TCAATACGGGTCTTGTGGAGCTGCTGTACGAAATGTGATGGCTTTTAAATGAAGAAG 180
    |||||||
Db  170  TCAATACGGGTCTTGTGGAGCTGCTGTACGAAATGTGATGGCTTTTAAATGAAGAAG 229

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Db  230  GAAGATGTTATGAACATTTTAGACTGGAACCAACAAAGCAATGTTGAAGTGCCTTTT 289

QY  241  TTCCCTGCCGTGTTCTTCAAGATTTTACTGGAATACCAGCAATGTTGATTTTGGT 300
    |||||||
Db  290  TTCCCTGCCGTGTTCTTCAAGATTTTACTGGAATACCAGCAATGTTGATTTTGGT 349

QY  301  GCTATGAGGAGCAGTGAAGTCTTTGGAGTGATCCTGAGAAAGTCCATCCTGTTGT 360
    |||||||
Db  350  GCTATGAGGAGCAGTGAAGTCTTTGGAGTGATCCTGAGAAAGTCCATCCTGTTGT 409

QY  361  CCAGACAGATCTACAGTTGACCATCTTTACAAATTTGACTTCAGTAAATGTCGAATACAG 420
    |||||||
Db  410  CCAGACAGATCTACAGTTGACCATCTTTACAAATTTGACTTCAGTAAATGTCGAATACAG 469

QY  421  AATGCACCAATCCTGGAGTGTGTGACCTGCAGAAAGCAGGAAAGCTCTCTCCACTTAA 480
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Db  470  AATGCACCAATCCTGGAGTGTGTGACCTGCAGAAAGCAGGAAAGCTCTCTCCACTTAA 529

QY  481  GTGAGCCTTAAGAAGCTTCCTGCAGAGGCCAGACTACCTGCCGAGGATCTTGTGATTC 540
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Db  530  GTGAGCCTTAAGAAGCTTCCTGCAGAGGCCAGACTACCTGCCGAGGATCTTGTGATTC 589

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Db  650  TGTCCCTTTTCATTTGCAACACAGTGCCTGAACTGAAACAGTGTATAAAATCAAGAAGTA 709

QY  661  GAATTCGGCAGAAATCGAGAGGCTTCAGTTTTTAAAGTGAAGTTCAAGATTTTAAAG 720
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Db  710  GAATTCGGCAGAAATCGAGAGGCTTCAGTTTTTAAAGTGAAGTTCAAGATTTTAAAG 769

QY  721  AATGTGGCAGTATCCTCTCGAACTGGAATGGCTCATCAATAAAGTGAAGTTTGA 780
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Db  770  AATGTGGCAGTATCCTCTCGAACTGGAATGGCTCATCAATAAAGTGAAGTTTGA 828

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RESULT 2

BM802385

LOCUS

DEFINITION

AGENCY

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QY 2879 AGTCACTCTCTCTATACCAATCTGAGACCATTTTCAATTTTGAAGAAAGACAAATAACATGG 2938
Db 477 AGTCACTCTCTCTATACCAATCTGAGACCATTTTCAATTTTGAAGAAAGACAAATAACATGG 536
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QY 3059 ATTTGGGCCAGTAGTTATATTTGAAAAATGTTTATAGCCAATATATATTTTATTTA 3118
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QY 3177 TAGCAACACAC- ---TGTTTATGCACTGCTAAGAAAGATAAAGGCTGTGTGCACT 3232
Db 777 GTTAGCACACACCACTGGTGTATTTGCACTGCTAAGAAAGATAAAGGCTGTGTG 836
QY 3233 G-----GCTCACACCTGTGGAGCGCAAGCGAGGAGCATCA- ---CTTAGGCGCA 3278
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DEFINITION
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ACCESSION
BG260015
VERSION
BG260015.1 GI:12769831
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1068)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10312 row: g column: 24
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Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 366 a 161 c 254 g 267 t
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Query Match 14.9%; Score 648.6; DB 12; Length 1068;
Best Local Similarity 85.9%; Pred. No. 5.8e-71;
Matches 779; Conservative 0; Mismatches 119; Indels 9; Gaps 5;
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QY 384 -TTCTTTACAAATGACTTTCAGTAAATGTGCAATACAGAAATGCACAAATCCTGGAGGTG 442
Db 181 GTTCTTTACAAATGACTTTCAGTAAATGTGCAATACAGAAATGCACAAATCCTGGAGGTG 240
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DEFINITION 602412909F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4521122 5',
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VERSION  BG387889
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM10420 row: b column: 03
          High quality sequence stop: 631.

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     /tissue_type="embryonal carcinoma, cell line"
     /lab_host="DH10B (phage-resistant)"
     /note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
     Average insert size 2.5 kb. Library enriched for
     full-length clones and constructed by Life Technologies.
     Note: this is a NIH_MGC Library."

BASE COUNT  300 a 250 c 195 g 193 t
ORIGIN
Query Match      14.4%; Score 626.8; DB 12; Length 938;
Best Local Similarity 90.9%; Pred. No. 3e-68;
Matches 700; Conservative 0; Mismatches 67; Indels 3; Gaps 3;

Qy 1 ATGAGCGCCCAAAAGCAGATACGCGCTTTGAGTACCTATTGAAACATTAATGACAGT 60
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Db 50 ATGAGCGCCCAAAAGCAGATACGCGCTTTGAGTACCTATTGAAACATTAATGACAGT 109
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Qy 61 TCACATAAAGAGTTCTTCATGTATCTAAACTTGGCACCAGATGATGTTGCGCTTAC 120
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Db 110 TCACATAAAGAGTTCTTCATGTATCTAAACTTGGCACCAGATGATGTTGCGCTTAC 169
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Qy 121 TCANTACGGGTCTTGTGGAAGCTGCTGTACGAAATTTGATGGCTTTTATGAAGAAG 180
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Db 170 TCANTACGGGTCTTGTGGAAGCTGCTGTACGAAATTTGATGGCTTTTATGAAGAAG 229
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Qy 181 GAAGATGTTATGAACATTTAGACATGGAAACCAACAAAGCAATGTTGAAGTGCCTTT 240
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Db 230 GAAGATGTTATGAACATTTAGACATGGAAACCAACAAAGCAATGTTGAAGTGCCTTT 289
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Qy 241 TTCCCTGCCCGTCTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTTCT 300
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Db      290  TTCCCTGCCCGTCTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTTGCT 349
Qy      301  GCTATGAGGGAGGAGTGAAGAACTCTTTGGAGGTGATCCTCGAGAAAGTCCATCTCGCTTGT 360
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Db      350  GCTATGAGGGAGGAGTGAAGAACTCTTTGGAGGTGATCCTCGAGAAAGTCCATCTCGCTTGT 409
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Qy      361  CCGACAGATCTTACAGTTGACCATCTTTTACAAATTTGACATTAATGTCGAATACAG 420
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Db      410  CCGACAGATCTTACAGTTGACCATCTTTTACAAATTTGACATTAATGTCGAATACAG 469
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Qy      421  AATGACCAAAATCTGGAGGTGGTACCTGCAGAAAGCAGGAAAGCTCTCTCCACTTAAA 480
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Db      470  AATGACCAAAATCTGGAGGTGGTACCTGCAGAAAGCAGGAAAGCTCTCTCCACTTAAA 529
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Qy      481  GTGCAGCCTTAAGAAAGCTTCCCTGCAGAGGCCAGACTACCTGCCGAGGATCTTGTGATTCT 540
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Qy      541  GGAGAACTVAGCCGGAACATCAGGAACATTTTCTCGAGATTTGAGATACACCCATCCTG 600
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Qy      660  AGAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTAAAGTGGAGTTCAAG-AGTTTTAA 718
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Db      709  ACACATCGGCCGACACATCGAGAAAGCCAGACACAGACAGAACTCAGCAAGTACAC 768
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Qy      719  AGAATGTGGCGATGATCCTCTCGAACTGGAATGGCTCATCAATAAATAC 768
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RESULT 5
LOCUS   BQ224816
DEFINITION AGENCOURT_7570815 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6058466
          5', mRNA sequence.
ACCESSION BQ224816
VERSION   BQ224816.1 GI:20406226
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-remail.nih.gov
          Tissue Procurement: DCTD/DTP/Gazdar
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM13323 row: j column: 03
          High quality sequence start: 93
          High quality sequence stop: 383.

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     /tissue_type="large cell carcinoma"
     /lab_host="DH10B (phage-resistant)"
     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
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Query Match	11.4%; Score 494.4; DB 14; Length 581;	
Best Local Similarity	95.9%; Pred. No. 7.3e-52;	
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Db		
560	GTTGGTACTGATGTTGTTTATACCCAGGAAATAATTTTNGAGGGGATTTAAGTTGA 501	
QY 2998	AACCACTGTTAA-CAAACTACCAAGTGGGATTCGCTGCTGATTAAGATGCTGTA 3056	
Db		
500	ACCCACATGTTAACCAANTTCTACCAAGTGGGATTTGCCGTGATTAAGATGCTGTA 441	
QY 3057	ACATTTGGG-CCAGTAGTATTAATTTGAAAATGTTTATACCA-ATATATAATTTT 3114	
Db		
440	ACATTTGGGCCCATGATTAATTTGAAAATGTTTATACCAATATATAATTTT 381	
QY 3115	TTTAATATACAGTTTCATCAGTCTATTAGTATTTCAATTAAGTCTAAGATGCCATCAGTG 3174	
Db		
380	TTTAATATACAGTTTCATCAGTCTATTAGTATTTCAATTAAGTCTAAGATGCCATCAGTG 321	
QY 3175	GTACCAACACCACTGTTTATGCACTGCTAAGAAAGTAAGGCTGCTGCACTGG 3234	
Db		
320	GTACCAACACCACTGTTTATGCACTGCTAAGAAAGTAAGGCTGCTGCACTGG 261	
QY 3235	CTCACACCTGTGGAGCCCAAGGAGGAGCATCCTTGAGGCCAGAAAGTTCAAGACCAAC 3294	
Db		
260	CTCACACCTGTGGAGCCCAAGGAGGAGCATCCTTGAGGCCAGAAAGTTCAAGACCAAC 201	
QY 3295	CTGGTCAACATGTAAGACCCCTGCTCTACAAAAAAGTAAGTAAAAATTAGCTGGGT 3354	
Db		
200	CTGGTCAACATGTAAGACCCCTGCTCTACAAAAAAGTAAGTAAAAATTAGCTGGGT 141	
QY 3355	GGGTTGGACATGCTGTAGTCTCAGCTACTCTGGAGGCTAAGGTGGAGGATGCTAGA 3414	
Db		
140	GGGTTGGACATGCTGTAGTCTCAGCTACTCTGGAGGCTAAGGTGGAGGATGCTAGA 81	
QY 3415	GCCACGGTGTGGAGCTGCAATGAGCTGTGACCAACACCACTGGCGTCCAGCGTGGGCAA 3474	
Db		
80	GCCACGGTGTGGAGCTGCAATGAGCTGTGACCAACACCACTGGCGTCCAGCGTGGGCAA 21	
QY 3475	CAGAGTGAGACCTGTTCT 3494	
Db		
20	CAGAGTGAGACCTGTTCT 1	
RESULT 9		
AA224499		
LOCUS	AA224499 509 bp mRNA linear EST 19-FEB-1997	
DEFINITION	zr16f03.r1 Stragene NT2 neuronal precursor 937230 Homo sapiens	
	cDNA clone IMAGE:563581 5' similar to TR:G897581 G897581	
	IRON-REGULATORY PROTEIN 2 ; mRNA sequence.	
ACCESSION	AA224499	
VERSION	AA224499.1 GI:1845041	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
REFERENCE	1 (bases 1 to 509)	
AUTHORS	Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,	
	Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins	
	M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore	
	B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,	
	Schellenberg, K., Soares, M.B., Tap, F., Thierry-Mieg, J., Trevisan, E.,	
	Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Warrar, M.	
	Generation and analysis of 280,000 human expressed sequence tags	
	Genome Res. 6 (9), 807-828 (1996)	
TITLE		
JOURNAL		
MEDLINE		
COMMENT	Contact: Wilson RK	
	Washington University School of Medicine	
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	
	Tel: 314 286 1800	
	Fax: 314 286 1810	

FEATURES	Source	
1..509	/organism="Homo sapiens"	
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	/note="Organ: brain; Vector: pBluescript SK-; Site: 1:	
	ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:	
	Oligo dT. Undiluted, exponentially growing neuroepithelial	
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	Uni-ZAP XE Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG	
	3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'.	
BASE COUNT	145 a 114 g 144 t 2 others	
ORIGIN		
Query Match	11.2%; Score 487.2; DB 9; Length 509;	
Best Local Similarity	99.0%; Pred. No. 6e-51;	
Matches 489; Conservative	0; Mismatches 5; Indels 0; Gaps 0;	
QY 36	CCTTATTGAAACATTAATGACAGTTTCACATAAGAGTTCTTCGATGATATCTAACTGG 95	
Db		
16	CTTATTGAAACATTAATGACAGTTTCACATAAGAGTTCTTCGATGATATCTAACTGG 75	
QY 96	CACCAAGTATGATGCTTCGCTTACTCAATACGAGTCTTTGGAGCTCCTCTACGAAA 155	
Db		
76	CACCAAGTATGATGCTTCGCTTACTCAATACGAGTCTTTGGAGCTCCTCTACGAAA 135	
QY 156	TTGTGATGGCTTTTAAATGAAGAGGAGATGTTATGAACATTTTAGACTGGAAAAACCA 215	
Db		
136	TTGTGATGGCTTTTAAATGAAGAGGAGATGTTATGAACATTTTAGACTGGAAAAACCA 195	
QY 216	ACAAAGCAATGTTGAAGTGCCTTTTCCCTGCGCTCTCTCTCAAGATTTTAACTGG 275	
Db		
196	ACAAAGCAATGTTGAAGTGCCTTTTCCCTGCGCTCTCTCTCAAGATTTTAACTGG 255	
QY 276	ATACAGCAATGTTGGATTTTGGCTCTATGAGGAGGAGTGAACACTCTTGAGGTGA 335	
Db		
256	AATACAGCAATGTTGGATTTTGGCTCTATGAGGAGGAGTGAACACTCTTGAGGTGA 315	
QY 336	TCCTGAGAAAGTCCATCCTCTTGTCCGACAGATCTTACAGTTGACCATTTCTTACAAAT 395	
Db		
316	TCCTGAGAAAGTCCATCCTCTTGTCCGACAGATCTTACAGTTGACCATTTCTTACAAAT 375	
QY 396	TGACTTCAGTAAATGTCATACAGATGCACCAATCCTCGAGTGCTGACCTGCAGAA 455	
Db		
376	TGACTTCAGTAAATGTCATACAGATGCACCAATCCTCGAGTGCTGACCTGCAGAA 435	
QY 456	AGCAGAAAGCTCTCTCCACTTAAAGTGCAGCTTAAAGTGCAGCTTCCCTGCAGAGCCAGAC 515	
Db		
436	AGCAGAAAGCTCTCTCCACTTAAAGTGCAGCTTAAAGTGCAGCTTCCCTGCAGAGCCAGAC 495	
QY 516	TACCTGCCGAGGAT 529	
Db		
496	TACCTGCCGAGGAT 509	
RESULT 10		
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LOCUS	AA104450 567 bp mRNA linear EST 29-OCT-1996	
DEFINITION	mo45a10.r1 Life Tech mouse embryo 15 5dpc 10667012 Mus musculus	
	cDNA clone IMAGE:556506 5' similar to gb:X61147 M.musculus mRNA for	
	iron responsive element binding (MOUSE);, mRNA sequence.	
ACCESSION	AA104450	
VERSION	AA104450.1 GI:1650611	

KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Marra, M., Kucuba, T., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Hillier, F., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wyllie, F., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE The WashU-HMMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LILN; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:337298
Seq primer: -28M13 rev1 from Amersham
High quality sequence stop: 466.

FEATURES
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Location/Qualifiers
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Matches 523; Conservative 0; Mismatches 44; Indels 1; Gaps 1;
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QY 465 GCTCTCTCCACTTAAAGTGCAGCTTAGAGAGCTTCCCTGCAGAGGCCAGACTACCTGCCG 524
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QY 525 AGGATCTGTGTGATCTCGGAGAACTAGGCCGAACTCAGGAACATTTCTTCGCGAGATTGA 584
DB 121 -GGATCTGTGTGATCTCGGAGAGCTTAAGCGGAATCTCAGGAACATTTCTTCACAGATTGA 179
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QY 765 AAATCTAGATATTTTCTCAAGAGTGGTTTTCGAAAGAAAAAGCTTCTCTTCCAGACAG 824
DB 360 GAATCTAGATATTTTCTCAAGAGTGGTTTTCGAAAGAAAAAGCTTCTCTTCCAGACAG 419

QY 825 TGTAGTCGCACAGATTACACATAACAGATGGTGAATGTTTGGGATTTGGGGTGGG 884
DB 420 TGTAGTCGCACAGATTCTCATATAACCATGTTGACGAGTTGGGGATTTCTTGGGTGGG 479
QY 885 GGTGTGAGCATTGAACAGAGCAGTTATGCTTGTGCTGCGCAGTTCCTTACTTTACC 944
DB 480 AGTTGTGCGCATTGAGACAGAGCAGTTATGCTTGTGCTGCGCAGTTCCTTACTTTACC 539
QY 945 AGAGGTGTTGGATGCTGAGTAACTGGG 972
DB 540 AGAGGTGTTGGATGCTGAGTAACTGGG 567

RESULT 11
AA313478
AA313478
LOCUS
DEFINITION
EST183363 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
similar to iron-responsive element-binding protein, mRNA sequence.
ACCESSION
AA313478
VERSION
AA313478.1 GI:1965807
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 498)
AUTHORS
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult
, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White
, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,
Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald
, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,
Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M.,
Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Wiley, J.,
Bednarek, D.P., Cao, L., Cepeda, W.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.,
, Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
Kunsch, C., Hungjun, J., Li, H., Meisner, P.S., Olsen, H., Raymond, L.,
Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon
, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
Venter, J.C.
TITLE
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280
Other ESTs: THCB5618
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tldb/hgi/hgi.html>)
Seq primer: M13 Reverse.
FEATURES
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/db_xref="taxon:9606"
/clone_lib="Colon carcinoma (HCC) cell line"
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EcoRI; Site:2: XhoI"
BASE COUNT 144 a 98 c 113 g 143 t
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Query Match	11.1%	Score 482.8	DB 9	Length 498
Best Local Similarity	99.6%	Pred. No. 2.1e-50		
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QY	61	TCACATAAGAAGTTCTTCGATGTATCTAAACTTGGCACCAAGTATGATGTCTGCCTTAC	120	
Db	73	TCACATAAGAAGTTCTTCGATGTATCTAAACTTGGCACCAAGTATGATGTCTGCCTTAC	132	
QY	121	TCAAATACGGCTCTGTTGGAAAGCTGCTGACGAAATGTGATGCGCTTTTAAATCAAGAAG	180	
Db	133	TCAAATACGGCTCTGTTGGAAAGCTGCTGACGAAATGTGATGCGCTTTTAAATCAAGAAG	192	
QY	181	GAAGATGTTATGAACATTTTATAGCTGGAAACCAACAAAGCAATGTGTGAAGTGCCTTT	240	
Db	193	GAAGATGTTATGAACATTTTATAGCTGGAAACCAACAAAGCAATGTGTGAAGTGCCTTT	252	
QY	241	TTCCCTGCCCGTCTCTTCTCAAGATTTTACTGGAATACCACGAATGGTGGATTTTGGCT	300	
Db	253	TTCCCTGCCCGTCTCTTCTTCAAGATTTTACTGGAATACCACGAATGGTGGATTTTGGCT	312	
QY	301	GCTATGAGGAGGACGAGTAAACTCTTGGAGGTGATCCTGAGAAAGTCCATCTGCTGTGT	360	
Db	313	GCTATGAGGAGGACGAGTAAACTCTTGGAGGTGATCCTGAGAAAGTCCATCTGCTGTGT	372	
QY	361	CGACAGATCTTACAGTTGACCATTCATTACAAATTGACTTCAGTAAATGGCAATACAG	420	
Db	373	CGACAGATCTTACAGTTGACCATTCATTACAAATTGACTTCAGTAAATGGCAATACAG	432	
QY	421	AATGCACCAATCTCGAGGTGGTGACCTGCAGAAAGCAGGAAGCTCTCTCCACTTAA	480	
Db	433	AATGCACCAATCTCGAGGTGGTGACCTGCAGAAAGCAGGAAGCTCTCTCCACTTAA	492	
QY	481	GTGCAG 486		
Db	493	GTGCAG 498		
RESULT 12				
LOCUS	AL121430	467 bp	mrna	linear EST 25-FEB-2000
DEFINITION	DRFZP7621247_r1_762 (synonym: hmel2) Homo sapiens cDNA clone			
ACCESSION	DRFZP7621247 5', mRNA sequence.			
VERSION	AL121430			
KEYWORDS	AL121430.1 GI:5927431			
SOURCE	EST.			
ORGANISM	human.			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	1 (bases 1 to 467)			
JOURNAL	Ottewaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.			
COMMENT	EST (Ottewaelder, et al.) Unpublished (1999) Contact: Ottewaelder B MIPS Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; sequenced by MedGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. No sl sequence available. This clone (DRFZP7621247) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers 1. .467			
FEATURES				
SOURCE				

